

FIGURE 1

GGGGCTTCGGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGGATTTACAAAAGGTGCAGGTATG
AGCAGGTCTGAAGACTAACATTTTGTGAAGTTGTAAAACAGAAAACCTGTTAGAAATGTGGTGGT
TTCAGCAAGGCCTCAGTTTCCTTCCTTCAGCCCTTGTAATTTGGACATCTGCTGCTTTTCATATTT
TCATACATTACTGCAGTAACACTCCACCATATAGACCCGGCTTTACCTTATATCAGTGACACTGG
TACAGTAGCTCCAGAAAAATGCTTATTTGGGGCAATGCTAAAATATTGCGGCAGTTTTATGCATTG
CTACCATTTATGTTTCGTTATAAGCAAGTTCATGCTCTGAGTCCTGAAGAGAACGTTATCATCAA
TTAAACAAGGCTGGCCTTGTACTTGAATACTGAGTTGTTTAGGACTTTCTATTGTGGCAAACCTT
CCAGAAAAACAACCCTTTTTGCTGCACATGTAAGTGGAGCTGTGCTTACCTTTGGTATGGGCTCAT
TATATATGTTTGTTCAGACCATCCTTTCTACCAAATGCAGCCCAAATCCATGGCAAACAAGTC
TTCTGGATCAGACTGTTGTTGGTTATCTGGTGTGGAGTAAGTGCACCTTAGCATGCTGACTTGCTC
ATCAGTTTGCACAGTGGCAATTTGGGACTGATTTAGAACAGAACTCCATTGGAACCCCGAGG
ACAAAGGTTATGTGCTTCACATGATCACTACTGCAGCAGAATGGTCTATGTCATTTTCCTTCTTT
GGTTTTTTCCTGACTTACATTCGTGATTTTCAGAAAATTTCTTTACGGGTGGAAGCCAATTTACA
TGGATTAACCCTCTATGACACTGCACCTTGCCCTATTAACAATGAACGAACACGGCTACTTTCCA
GAGATATTTGATGAAAGGATAAAATATTTCTGTAATGATTATGATTCTCAGGGATTGGGGAAAGG
TTCACAGAAGTTGCTTATTCTTCTCTGAAATTTTCAACCCTTAATCAAGGCTGACAGTAACACT
GATGAATGCTGATAATCAGGAAACATGAAAGAAGCCATTTGATAGATTATTCTAAAGGATATCAT
CAAGAAGACTATTAAAAACACCTATGCCTATACTTTTTTATCTCAGAAAATAAAGTCAAAAGACT
ATG

FIGURE 2

<subunit 1 of 1, 266 aa, 1 stop

<MW: 29766, pI: 8.39, NX(S/T): 0

MWWFQQGLSFLPSALVIWTSAAFI FSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNIAAV
LCIATIIYVRYKQVIHALSPEENVIIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVSGAVLTFG
MGSLYMFVQTIILSYMQPKIHGKQVFWIRLLLVWCGVSALSMLTCSSVLHSGNFGTDLEQKLHW
NPEDKGYVLHMITTAAEWSMSFSFFGFFLTYYIRDFQKISLRVEANLHGLTLYDTAPCPINNERTR
LLSRDI

Important features:

Type II transmembrane domain:

amino acids 13-33

Other Transmembrane domains:

amino acids 54-73, 94-113, 160-180, 122-141

N-myristoylation sites.

amino acids 57-63, 95-101, 99-105, 124-130, 183-189

FIGURE 3

CGGACGCGTGGGCGGACGCGTGGGGGAGAGCCGACGTCCCGGCTGCAGCACCTGGGAGAAGGCAGACC
GTGTGAGGGGGCCTGTGGCCCCAGCGTGTGTGGCCTCGGGGAGTGGGAAGTGGAGGCAGGAGCCTTC
CTTACACTTCGCCATGAGTTTCCTCATCGACTCCAGCATCATGATTACCTCCAGATACTATTTTTTG
GATTGGGTGGCTTTTCTTCATGCGCCAATTGTTTAAAGACTATGAGATACGTCAGTATGTTGTACAG
GTGATCTTCTCCGTGACGTTTGCAATTTCTTGCAACCATGTTTGAGCTCATCATCTTTGAAATCTTAGG
AGTATTGAATAGCAGCTCCCGTTATTTTCACTGGAAAATGAACCTGTGTGAATTCTGCTGATCCTGG
TTTTCATGGTGCCTTTTTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCATAAACACGA
CTGCTTTTTTCTGTCTCTTATGGCTGACCTTTATGTATTTCTTCTGGAACTAGGAGATCCCTTTCC
CATTCTCAGCCCAAACATGGGATCTTATCCATAGAACAGCTCATCAGCCGGGTGGTGTGATTGGAG
TGACTCTCATGGCTCTTCTTCTGGATTGGTGTCTGCAACTGCCCATACACTTACATGTCTTACTTC
CTCAGGAATGTGACTGACACGGATATCTAGCCCTGGAACGGCGACTGCTGCAAACCATGGATATGAT
CATAAGCAAAAAGAAAAGGATGGCAATGGCACGGAGAACAATGTTCCAGAAGGGGGAAGTGCATAACA
AACCATCAGGTTTCTGGGAATGATAAAAAGTGTACCCTTCAGCATCAGGAAGTGAATCTTACT
CTTATTCAACAGGAAGTGGATGCTTTGGAAGAATTAAGCAGGCAGCTTTTTCTGGAAACAGCTGATCT
ATATGCTACCAAGGAGAGAATAGAATACTCCAAAACCTTCAAGGGGAAATATTTTAATTTCTTGGTT
ACTTTTTCTCTATTTACTGTGTTTGGAAAATTTTCATGGCTACCATCAATATTGTTTTTGATCGAGTT
GGGAAAACGGATCCTGTCAAGAGGCATTGAGATCACTGTGAATTATCTGGGAATCCAATTTGATGT
GAAGTTTTGGTCCCAACACATTTCTTCATTCTGTTGGAATAATCATCGTCACATCCATCAGAGGAT
TGCTGATCACTCTTACCAAGTTCTTTTATGCCATCTCTAGCAGTAAGTCTCCAATGTCAATTGTCTTG
CTATTAGCACAGATAATGGGCATGTACTTTGTCTCCTCTGTGCTGATCCGAATGAGTATGCCTTT
AGAATACCGCACCATAATCACTGAAGTCCTTGGAGAAGTGCAGTTCAACTTCTATCACCGTTGGTTTG
ATGTGATCTTCTGGTCAGCGCTCTCTAGCATACTCTTCTCTATTTGGCTCACAAACAGGCACCA
GAGAAGCAAATGGCACCTTGAACTTTAAGCCTACTACAGACTGTTAGAGGCCAGTGGTTTTCAAAATTTA
GATATAAGAGGGGGGAAAAATGGAACCGGGCCTGACATTTTATAAACAAACAAAATGCTATGGTAGC
ATTTTTTACCTTCATAGCATACTCTTCCCCGTGAGGTGATACTATGACCATGAGTAGCATCAGCCAG
AACATGAGAGGGAGAACTAACTCAAGACAATACTCAGCAGAGAGCATCCCGTGTGGATATGAGGCTGG
TGTAGAGGCGGAGAGGAGCCAAGAACTAAAGGTGAAAAATACACTGGAACCTCTGGGGCAAGACATGT
CTATGGTAGCTGAGCCAAACACGTAGGATTTCCGTTTTAAGGTTTACATGGAAGGTTATAGCTTTG
CCTTGAGATTGACTCATTTAAATCAGAGACTGTAACAAAAAAGGGCGGCCGCG
ACTCTAGAGTCGACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGTTTATTGCAGCTTATAATG

FIGURE 5

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATAGTTCC
 AGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGCCATCTGAGGT
 GTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACT
 TCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGT
 GTCATGCAGAATTATGGGGATCACCCTTGTGAGCAAAAAGGCGAACCAGCAGCTGAATTTACAG
 AAGCTAAGGAGGCCGTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCC
 TTGAAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGGTTGGAGATGGATTTCGTGGTCATCTCTAG
 GATTAGCCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGCTTGATTTGGAAGGTTCCAGTGA
 GCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTGCATTCCAGAA
 ATTATCACCACCAAGATCCCATATTCAACACTCAAACGCAACACAAACAGAAATTTATTGT
 CAGTGACAGTACCTACTCGGTGGCATCCCCCTTACTCTACAATACCTGCCCTACTACTACTCCTC
 CTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTTGTGTACAGAAAGTTTATG
 GAACTAGCACCATGTCTACAGAACTGAACCATTTGTTGAAAAAAGCAGCATTCAAGAATGA
 AGCTGTGGGTTTGGAGGTGTCCACGGCTCTGCTAGTGTCTGCTCTCCTCTCTTTGGTGCTG
 CAGCTGGTCTTGGATTTTGCTATGTCAAAAGGTATGTGAAGGCCCTCCCTTTTACAAACAAGAA
 CAGCAGAAGGAAATGATCGAAACCAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCTAA
 TGAGGAATCAAAGAAAAGTATAAAACCCAGAAAGAGTCCAGAGTCCAAAGCAAAACTACCGTGC
 GATGCCTGGAAGCTGAAGTTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTTCTTT
 CATGCTCCTTACCCTGCCCCAGCTGGGGAAATCAAAGGGCCAAAGAACCAAGAAGAAAGTCCA
 CCCTTGGTTCCTAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAA
 GCCCTTCTCCTTATTGTAACCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCACGGCCT
 TTCTAGCCTGGCTATGTCTAATAATATCCCACTGGGAGAAAGGAGTTTGCAAAGTGAAGGAC
 CTAAAAATCTCATCAGTATCCAGTGGTAAAAAGGCCCTCCTGGCTGTCTGAGGCTAGGTGGGTTG
 AAAGCCAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCCGCAGCTCAGACCCTTTCTTCA
 GCTCTGAAAGAGAAACACGTATCCACCTGACATGTCCTTCTGAGCCCGGTAAGAGCAAAAGAA
 GGCAGAAAAGTTAGCCCCGTAAGCCATGGAGATTCTCATAACTTGAGACCTAATCTCTGTAAA
 GCTAAATAAAGAAATAGAACAAGGCTGAGGATACGACAGTACACTGTCTGAGGAGGACTGTAAAC
 ACAGACAGGGTCAAAGTGTTTTCTCTGAACACATTGAGTTGGAATCACTGTTTAGAACACACACA
 CTTACTTTTTCTGGTCTCTACCACTGCTGATATTTCTCTAGGAAATATACTTTTACAAGTAACA
 AAAATAAAAACTCTTATAAATTTCTATTTTATCTGAGTTACAGAAATGATTACTAAGGAAGATT
 ACTCAGTAATTTGTTAAAAAGTAATAAAATTCACAAACATTTGCTGAATAGCTACTATATGTC
 AAGTGTGTGCAAGGTATTACACTCTGTAATTGAATATTATTCCTCAAAAAATTGCACATAGTAG
 AACGCTATCTGGGAAGCTATTTTTTTCAGTTTTGATATTTCTAGCTTATCTACTTCCAACTAAT
 TTTTATTTTGTGCTGAGACTAATCTTATTCATTTTCTCTAATATGGCAACCATTATAACCTTAATT
 TATTATTAACATACCTAAGAAGTACATTGTTACCTCTATATACCAAGCACATTTTAAAGTGCC
 ATTAACAAATGTATCACTAGCCCTCCTTTTTTCCAACAAGAAGGACTGAGAGATGCAGAAATATT
 TGTGACAAAAAATTAAAGCATTTAGAAAACTT

FIGURE 6

MARCFSLVLLLSIWTRLLVQGSRLAEELSIQVSCRIMGITLVSKKANQQLNFTAKEACRLLG
 LSLAGKDQVETALKASFETCSYGWVGDFVVISRISPNPKCGKNGVGVLWKVPVSRQFAAYCYN
 SSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPAPASTSIPR
 RKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTALLVLALLFFGAAAGLGFCYVK
 RYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSPSKTTVRCLEAEV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 53-57, 130-134, 289-293

Casein kinase II phosphorylation site.

amino acids 145-149, 214-218

Tyrosine kinase phosphorylation site.

amino acids 79-88

N-myristoylation site.

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

FIGURE 7

CGCCGCGCTCCCGCACCCGCGGCCCGCCACCGCGCCGCTCCCGCATCTGCACCCGCAGCCCGGC
GGCCTCCCGGCGGGAGCGAGCAGATCCAGTCCGGCCCCGAGCGCAACTCGGTCCAGTCCGGGCGG
CGGCTGCGGGCGCAGAGCGGAGATGACGCGGCTTGGGGCCACCCTGCTGTGCCTGCTGCTGGCGG
CGGCGGTCCCCACGGCCCCCGCGCCGCTCCGACGGCGACCTCGGCTCCAGTCAAGCCCGGCCG
GCTCTCAGCTACCCGCAGGAGGAGGCCACCCTCAATGAGATGTTCCGCGAGGTTGAGGAAGTAT
GGAGGACACGCAGCACAAATTGCGCAGCGCGGTGGAAGAGATGGAGGCAGAAGAAGCTGCTGCTA
AAGCATCATCAGAAGTGAACCTGGCAAACCTTACCTCCAGCTATCACAATGAGACCAACACAGAC
ACGAAGGTTGGAATAATACCATCCATGTGCACCGAGAAATTACAAGATAACCAACAACAGAC
TGGACAAATGGTCTTTTCAGAGACAGTTATCACATCTGTGGGAGACGAAGAAGGCAGAAGGAGCC
ACGAGTGCATCATCGACGAGGACTGTGGGCCAGCATGTACTGCCAGTTTGCCAGCTTCCAGTAC
ACCTGGCAGCCATGCCGGGGCCAGAGGATGCTCTGCACCCGGGACAGTGAAGTGTGTGGAGCCG
GCTGTGTGTCTGGGGTCACTGCACCAAAATGGCCACCAGGGGCAGCAATGGGACCATCTGTGACA
ACCAGAGGGACTGCCAGCCGGGGCTGTGCTGTGCCTTCCAGAGAGGCTGTGTTCCCTGTGTGC
ACACCCCTGCCCCGTGGAGGGCGAGCTTGGCCATGACCCCGCCAGCCGGCTTCTGGACCTCATCAC
CTGGGAGCTAGAGCCTGATGGAGCCTTGGACCGATGCCCTTGTGCCAGTGGCCTCCTCTGCCAGC
CCCACAGCCACAGCCTGGTGTATGTGTGAAGCCGACCTTCGTGGGGAGCCGTGACCAAGATGGG
GAGATCCTGTGCTGCCAGAGAGGTCCCGATGAGTATGAAGTTGGCAGCTTTCATGGAGGAGGTGG
CCAGGAGCTGGAGGACCTGGAGAGGAGCCTGACTGAAGAGATGGCGCTGGGGGAGCCTGCGGCTG
CCGCCGCTGCACTGCTGGGAGGGGAAGAGATTAGATCTGGACCAGGCTGTGGGTAGATGTGCAA
TAGAAATAGCTAATTTATTTCCCGAGGTGTGTGCTTTAGGCGTGGGCTGACCAGGCTTCTTCCTA
CATCTTCTTCCAGTAAGTTTCCCTCTGGCTTGACAGCATGAGGTGTTGTGCATTTGTTAGCT
CCCCCAGGCTGTTCTCCAGGCTTCACAGTCTGGTGCTTGGGAGAGTCAGGCAGGGTTAACTGCA
GGAGCAGTTTGCCACCCCTGTCCAGATTATTGGCTGCTTTGCCTTACCAGTTGGCAGACAGCCG
TTTGTCTACATGGCTTTGATAATTGTTTGAGGGGAGGAGATGGAAACAATGTGGAGTCTCCCTC
TGATTGGTTTTGGGGAAATGTGGAGAAGAGTGCCCTGCTTTGCAACATCAACCTGGCAAAATG
CAACAAATGAATTTTCCACGCAGTTCTTCCATGGGCATAGGTAAGCTGTGCCTTCAGCTGTTGC
AGATGAAATGTTCTGTTCACCCTGCATTACATGTGTTTATTCATCCAGCAGTGTGCTCAGCTCC
TACCTCTGTGCCAGGGCAGCATTTTCATATCCAAGATCAATTCCTCTCTCAGCACAGCCTGGGG
AGGGGGTCAATTGTTCTCCTCGTCCATCAGGGATCTCAGAGGCTCAGAGACTGCAAGCTGCTTGCC
CAAGTCACACAGCTAGTGAAGACCAGAGCAGTTTCATCTGGTTGTGACTCTAAGCTCAGTGCTCT
CTCCACTACCCACACCAGCCTTGGTGCCACCAAAAGTGCTCCCCAAAAGGAAGGAGAATGGGAT
TTTTCTTGAGGCATGCACATCTGGAATTAAGGTCAAATAATTCTCACATCCCTCTAAAAGTAA
CTACTGTTAGGAACAGCAGTGTCTCACAGTGTGGGGCAGCCGTCTTCTAATGAAGACAATGAT
ATTGACACTGTCCCTCTTTGGCAGTTGCATTAGTAACTTTGAAAGGTATATGACTGAGCGTAGCA
TACAGGTAACTGCAGAAACAGTACTTAGGTAATTGTAGGGCGAGGATTATAAATGAAATTTGC
AAAATCACTTAGCAGCAACTGAAGACAATTATCAACCACGTGGAGAAAATCAAACCGAGCAGGGC
TGTGTGAAACATGGTTGTAATATGCGACTGCGAACACTGAACCTCTACGCCACTCCACAAATGATG
TTTTCAGGTGTGATGGACTGTTGCCACCATGTATTCATCCAGAGTCTTAAAGTTTAAAGTTGCA
CATGATTGTATAAGCATGCTTTCTTTGAGTTTTAAATTATGTATAAACATAAGTTGCATTTAGAA
ATCAAGCATAAATCACTTCAACTGCAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 8

MQRLGATLLCLLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDTQHKL
 RSAVEEMEAEAAAKASSEVNLANLPSPYHNETNTDTKVGNNTIHVHREIHKITNNQTGQMVFSE
 TVITSVGDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRGQRMCLTRDSECCGDQLCVWGHC
 TKMATRGSNGTICDNQRDCQPGLCFAFQRLFFVCTPLPVEGELCHDPASRLDLITWELEPDG
 ALDRPCASGLLCQPHSHSLVYVCKPTFVGSRDQGEIILLPREVPDEYEVGSFMEEVRQELEDLE
 RSLTEEMALGEPAAAAAALLGGEI

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 96-100, 106-110, 121-125, 204-208

Casein kinase II phosphorylation site.

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,
 327-331

N-myristoylation site.

amino acids 202-208, 217-223

Amidation site.

amino acids 140-144

FIGURE 9

CGGACGCGTGGGCGGACGCGTGGGGGCTGTGAGAAAGTGCCAATAAATACATCATGCAACCCCAC
 GGCCACCTTGTGAACCTCTCGTGCCAGGGCTGATGTGCGTCTTCAGGGCTACTCATCCAAAG
 GCCTAATCCAACGTTCTGTCTTCAATCTGCAAATCTATGGGGTCTGGGGCTCTTCTGGACCCTT
 AACTGGGTACTGGCCCTGGGCCAATGCGTCCTCGCTGGAGCCTTTGCCTCCTTACTGGGCCTT
 CCACAAGCCCCAGGACATCCCTACCTTCCCCTTAATCTCTGCCTTCATCCGCACACTCCGTTACC
 AACTGGGTACTGGGCATTTGGAGCCCTCATCCTGACCCCTTGTGCAGATAGCCCGGGTCACTTG
 GAGTATATTGACCACAAGCTCAGAGGAGTGCAAGCCCTGTAGCCCGCTGCATCATGTGCTGTTT
 CAAGTGTGCTCTGGTGTCTGGAAAAATTTATCAAGTTCCTAAACCGCAATGCATACATCATGA
 TCGCCATCTACGGGAAGAATTTCTGTGTCTCAGCCAAAAATGCGTTCATGCTACTCATGCGAAAC
 ATTGTGAGGGTGGTCTCTGGACAAAGTCACAGACCTGCTGCTGTTCTTTGGGAAGCTGCTGGT
 GGTCGGAGGCGTGGGGTCTGTCTTCTTTTTTTCTCCGGTCGCATCCCGGGGCTGGGTAAAG
 ACTTTAAGAGCCCCACCTCAACTATTACTGGCTGCCCATCATGACCTCCATCCTGGGGGCTAT
 GTCATCGCCAGCGGCTTCTTCAGCGTTTTCGGCATGTGTGTGGACACGCTCTTCTCTGCTTCTT
 GGAAGACCTGGAGCGGAACAACGGCTCCCTGGACCGGCCCTACTACATGTCCAAGAGCCTTCTAA
 AGATTCTGGGCAAGAAGAACGAGGCGCCCCCGGACAACAAGAAGAGGAAGAAGTGACAGCTCCGG
 CCCTGATCCAGGACTGCACCCACCCCAACCGTCCAGCCATCCAACCTCACTTCGCCCTTACAGGT
 CTCCATTTTGTGGTAAAAAAGGTTTTAGGCCAGGCGCGTGGCTCACGCCTGTAATCCAACACT
 TTGAGAGGCTGAGGCGGGCGGATCACCTGAGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGTG
 AAACCTCCGTCTCTATTAAAAATACAAAAATTAGCCGAGAGTGGTGGCATGCACCTGTATCCCA
 GCTACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTGAGCCGA
 GATCGCGCCACTGCACTCCAACCTGGGTGACAGACTCTGTCTCCAAAACAAAACAAACAAA
 AAGATTTTATTAAAGATATTTTGTAACTC

FIGURE 10

RTRGRTRGGCEKVPINTSCNP'TAHLVNSSCPGLMCVFQGYSSKGLIQRSVFNLQIYGVLGLFWTL
 NWVLALGQCVLGAFASFYWAFHKPQDIPTFPLISAFIRTLRYHTGSLAFGALILTLVQIARVIL
 EYIDHKLRGVQNPVARCIMCCFKCCLWCLEKFIKFLNRNAYIMIAIYGKNFCVSAKNAFMLLMRN
 IVRVVLDKVTDLLFFGKLLVVGGVLSFFFFSGRIPGLGKDFKSPHLNYYWLPIMTSILGAY
 VIASGFFSVFGMCVDTLFLCFLEDLERNNGSLDRPYMSKSLKILGKKNEAPPDNKKRKK

Important features:

Transmembrane domains:

amino acids 57-80 (type II), 110-126, 215-231, 254-274

N-glycosylation sites.

amino acids 16-20, 27-31, 289-293

Hypothetical YBR002c family proteins.

amino acids 276-288

Ammonium transporters proteins.

amino acids 204-231

N-myristoylation sites.

amino acids 60-66, 78-84

Amidation site.

amino acids 306-310

CCCCCCCCCCCCCCCC

FIGURE 12

MGACLGACSLSCASCLCGSAPCILSCCPASRNSTVSRLI FTFFLFLGVLVSIIMLSPGVESQL
YKLPWVCEEGAGIPTVLQGHIDCGSLGYPVYRMCFATAAFFFFFFFFTLLMLCVSSSRDPRAAIQ
NGFWFFKFLILVGLTVGAIFYIPDGSFTNIWFYFGVVGSLFLILQLVLLIDFAHSWNQRWLKAE
ECDSRAWYAGLFFFTLLFYLLSIAAVALMFMYYTEPSGCHEGKVFISLNLTFVCVVSIAAVLPKV
QDAQPNSGLLQASVITLYTMFVTWSALSSIPEQKCNPHLPTQLGNETVVAGPEGYETQWWDAPSI
VGLIIFLLCTLFISLRSSDHRQVNSIMQTEECPPMLDATQOQQQQVAACEGRAFDNEQDGVTSY
SFFHFCLVLASLHVMMTLTNWYKPGETRKMISTWTAVVVKICASWAGLLLYLWTLVAPLLLRNRD
FS

Signal sequence:

amino acids 1-20

Transmembrane domains:

amino acids 40-58, 101-116, 134-150, 162-178, 206-223, 240-257,
272-283, 324-340, 391-406, 428-444

FIGURE 14

MNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRFTCLFVTFDLLF
 VTLLWIIELNVNGGIENTLEKEVMQYDYSSYFDIFLLAVFRFKVLILAYAVCRLRHWWAIALTT
 AVTSAFLLAKVILSKLFSQGAFGYVLPPIISFILAWIETWFLDFKVLQPQAEENRLLIVQDASER
 AALIPGGLSDGQFYSPPESEAGSEEAEEKQDSEKPLLEL

Important features of the protein:-

Signal peptide:

amino acids 1-20

Transmembrane domains:

amino acids 54-72, 100-118, 130-144, 146-166

N-myristoylation sites.

amino acids 14-20, 78-84, 79-85, 202-208, 217-223

FIGURE 15

ACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCTCGGGCCCCGACCCGCCAGGAAAGACTGAGG
CCGCGGCTGCCCCGCGGCTCCCTGCGCGCGCGCGCTCCCGGGACAGAAGATGTGCTCCAG
GGTCCCTCTGCTGCTGCGGCTGCTCCTGCTACTGGCCCTGGGGCTGGGGTGCAGGGCTGCCCAT
CCGGCTGCCAGTGCAGCCAGCCACAGACAGTCTTCTGCACTGCCCGCCAGGGGACCACGGTGGCC
CGAGACGTGCCACCCGACACGGTGGGGCTGTACGTCTTTGAGAACGGCATCACCATGCTCGACGC
AGGCAGCTTTGCCGGCTGCCGGGCTGCAGCTCCTGGACCTGTCACAGAACCAGATCGCCAGCC
TGCCAGCGGGGTCTTCCAGCCACTCGCCAACCTCAGCAACCTGGACCTGACGGCCAACAGGCTG
CATGAAATCACCAATGAGACCTTCCGTGGCCTGCGGCGCCTCGAGCGCCTCTACCTGGGCAAGAA
CCGCATCCGCCACATCCAGCCTGGTGCCTTCGACACGCTCGACCGCCTCCTGGAGCTCAAGCTGC
AGGACAACGAGCTGCGGGCACTGCCCCGCTGCGCCTGCCCCGCTGCTGCTGCTGGACCTCAGC
CACAACAGCCTCCTGGCCCTGGAGCCCGGCATCCTGGACACTGCCAACGTGGAGGCGCTGCGGCT
GGCTGGTCTGGGGCTGCAGCAGCTGGACGAGGGGCTCTTCAGCGCTTGCGCGACCTCCACAGC
TGGATGTGTCCGACAACCAGCTGGAGCGAGTGCCACCTGTGATCCGAGGCCTCCGGGGCTGACG
CGCCTGCGGCTGGCCGGCAACACCCGCTATTGCCAGCTGCGGCGCGAGGACCTGGCCGGCTGGC
TGCCCTGCGAGGCTGGATGTGAGCAACCTAAGCCTGCAGGCCCTGCTGGCGACCTCTCGGGCC
TCTTCCCCGCTGCGGCTGCTGGCAGCTGCCCGCAACCCCTTCAACTGCGTGTGCCCCCTGAGC
TGGTTTGGCCCCCTGGGTGCGCGAGAGCCACGTACACTGGCCAGCCCTGAGGAGACGCGCTGCCA
CTTCCCGCCCAAGAAGCTGGCCGGCTGCTCCTGGAGCTTGACTACGCCGACTTTGGCTGCCCAG
CCACCACCACACAGCCACAGTGCCACACAGAGGCCCGTGGTGGCGGAGCCACAGCCTTGTCT
TCTAGCTTGGCTCCTACCTGGCTTAGCCCCACAGCGCCGGCCACTGAGGCCCCAGCCCGCCCTC
CACTGCCCCACCGACTGTAGGGCCTGTCCCCAGCCCCAGGACTGCCACCCCTCCACCTGCCCTCA
ATGGGGGCACATGCCACCTGGGGACACGGCACCTGGCGTGTGTGCCCCGAAGGCTTCACG
GGCCTTACTGTGAGAGCCAGATGGGGCAGGGGACACGGCCAGCCCTACACAGTCACGCCGAG
GCCACCACGGTCCCTGACCCTGGGCATCGAGCCGGTGAGCCCCACCTCCCTGCGCGTGGGGCTGC
AGCGTACCTCCAGGGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTATCGCAACCTATCG
GGCCCTGATAAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGCTGAGTACACGGTACCCCA
GCTGCGGCCCCAACGCCACTTACTCCGTCTGTGTATGCCTTTGGGGCCCGGGCGGGTGGCCGAGG
GCGAGGAGGCTGCGGGGAGGCCCATACCCCCAGCCGCTCCACTCCAACCACGCCCCAGTCACC
CAGGCCCCGCGAGGGCAACCTGCCGCTCCTCATTTGCGCCCCGCTGGCCGCGGTGCTCCTGGCCG
GCTGGCTGCGGTGGGGGACGCTACTGTGTGCGCGGGGGGCGGGCCATGGCAGCAGCGGCTCAGG
ACAAAGGGCAGGTGGGGCCAGGGGCTGGGCCCTGGAAGTGGAGGGAGTGAAGGTCCCTTTGGAG
CCAGGCCCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTGCCAGCGGGTCTGAGTGTGAGGTGCC
ACTCATGGGCTTCCAGGGCCTGGCCTCCAGTACCCCTCCACGCAAAGCCCTACATCTAAGCCA
GAGAGAGACAGGGCAGCTGGGGCCGGGCTCTCAGCCAGTGAGATGGCCAGCCCCCTCCTGCTGCC
ACACCACGTAAGTTCTCAGTCCCAACCTCGGGGATGTGTGACAGAGGGCTGTGTGACCACAGCT
GGGCCCTGTTCCCTTGGACCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCAGCTGACGAGCC
CTAACGTCCCCAGAACCGAGTGCCATGAGGACAGTGTCGCGCTGCCCTCCGCAACGTGCAGTC
CCTGGGCACGGCGGGCCCTGCCATGTGCTGGTAACGCATGCCCTGGGTCTGCTGGGCTCTCCAC
TCCAGCGGACCCCTGGGGGCCAGTGAAGGAAGCTCCCGAAAGAGCAGAGGGAGAGCGGGTAGGC
GGCTGTGTGACTCTAGTCTTGGCCCCAGGAAGCGAAGGAACAAAAGAACTGGAAAGGAAGATGC
TTTAGGAACATGTTTGTCTTTTTTAAATATATATATTTATAAGAGATCCTTTCCCATTTATCT
GGGAAGATGTTTTCAAACCTCAGAGACAAGGACTTTGGTTTTTGTAAAGACAACGATGATATGAA
GGCCTTTTGTAAAGAAAAATAAAGATGAAGTGTGAAA

FIGURE 16

MCSRVP LLLPL LLL L L L L L A L G P G V Q G C P S G C Q C S Q P Q T V F C T A R Q G T T V P R D V P P D T V G L Y V F E N G I T
 M L D A G S F A G L P G L Q L L D L S Q N Q I A S L P S G V F Q P L A N L S N L D L T A N R L H E I T N E T F R G L R R L E R L Y
 L G K N R I R H I Q P G A F D T L D R L L E L K L Q D N E L R A L P P L R L P R L L L L D L S H N S L L A L E P G I L D T A N V E
 A L R L A G L G L Q L D E G L F S R L R N L H D L D V S D N Q L E R V P P V I R G L R G L T R L R L A G N T R I A Q L R P E D L
 A G L A A L Q E L D V S N L S L Q A L P G D L S G L F P R L R L L A A R N P F N C V C P L S W F G P W V R E S H V T L A S P E E
 T R C H F P P K N A G R L L L E L D Y A D F G C P A T T T T A T V P T T R P V V R E P T A L S S S L A P T W L S P T A P A T E A P
 S P P S T A P P T V G P V P Q P Q D C P P S T C L N G G T C H L G T R H H L A C L C P E G F T G L Y C E S Q M G Q G T R P S P T P
 V T P R P P R S L T L G I E P V S P T S L R V G L Q R Y L Q G S S V Q L R S L R L T Y R N L S G P D K R L V T L R L P A S I A E Y
 T V T Q L R P N A T Y S V C V M P L G P G R V P E G E E A C G E A H T P P A V H S N H A P V T Q A R E G N L P L L I A P A L A A V
 L L A A L A A V G A A Y C V R R G R A M A A A A Q D K G Q V G P G A G P L E L E G V K V P L E P G P K A T E G G G E A L P S G S E
 C E V P L M G F P G P G L Q S P L H A K P Y I

Important features:

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 579-599

EGF-like domain cysteine pattern signature.

amino acids 430-442

Leucine zipper pattern.

amino acids 197-219, 269-291

N-glycosylation sites.

amino acids 101-105, 117-121, 273-277, 500-504, 528-532

Tyrosine kinase phosphorylation sites.

amino acids 124-131, 337-345

N-myristoylation sites.

amino acids 23-29, 27-33, 70-76, 142-148, 187-193, 348-354,
 594-600, 640-646

FIGURE 17

GCAGCGGCGAGGCGGCGGTGGTGGCTGAGTCCGTGGTGGCAGAGGCGAAGGCGACAGCTCATGCG
 GGTCCGGATAGGGCTGACGCTGCTGCTGTGTGCGGTGCTGCTGAGCTTGGCCTCGGCGTCTCGG
 ATGAAGAAGGCAGCCAGGATGAATCCTTAGATTCCAAGACTACTTTGACATCAGATGAGTCAGTA
 AAGGACCATACTACTGCAGGCAGAGTAGTTGCTGGTCAAATATTTCTTGATTGAGAAGAATCTGA
 ATTAGAATCCTCTATTCAAGAAGAGGAAGACAGCCTCAAGAGCCAAGAGGGGGAAAGTGTACAG
 AAGATATCAGCTTTCTAGAGTCTCCAAATCCAGAAAACAAGGACTATGAAGAGCCAAAGAAAGTA
 CGGAAACCAGCTTTGACCGCCATTGAAGGCACAGCACATGGGGAGCCCTGCCACTTCCCTTTTCT
 TTTCTAGATAAGGAGTATGATGAATGTACATCAGATGGGAGGGAAGATGGCAGACTGTGGTGTG
 CTACAACTTATGACTACAAAGCAGATGAAAAGTGGGGCTTTTGTGAACTGAAGAAGAGGCTGCT
 AAGAGACGGCAGATGCAGGAAGCAGAAATGATGTATCAAACCTGGAATGAAAATCCTTAATGGAAG
 CAATAAGAAAAGCCAAAAAAGAGAAGCATATCGGTATCTCCAAAAGGCAGCAAGCATGAACCATA
 CCAAAGCCCTGGAGAGAGTGTATATGCTCTTTTATTTGGTGATTACTTGCCACAGAATATCCAG
 GCAGCGAGAGAGATGTTTGAGAAGCTGACTGAGGAAGGCTCTCCCAAGGGACAGACTGCTCTTGG
 CTTTCTGTATGCCTCTGGACTTGGTGTTAATTCAGTCAGGCAAAGGCTCTTGATATTATACAT
 TTGGAGCTCTTGGGGGCAATCTAATAGCCCACATGGTTTTGGTAAGTAGACTTTAGTGGGAAGGCT
 AATAATATTAACATCAGAAGAATTTGTGGTTTATAGCGGCCACAACTTTTTCAGCTTTTCATGATC
 CAGATTTGCTTGTATTAAGACCAATATTCAGTTGAACTTCCTTCAAATCCTTGTTAATGGATAT
 AACACATGGAATCTACATGTAAATGAAAGTTGGTGGAGTCCACAATTTTCTTTAAATGATTAG
 TTTGGCTGATTGCCCCATAAAAGAGAGATCTGATAAATGGCTCTTTTTAAATTTTCTCTGAGTTG
 GAATTGTCAGAATCATTTTTTACATTAGATTATCATAATTTTAAAAATTTTCTTTAGTTTTTCA
 AAATTTTGTAATGGTGGCTATAGAAAAACAACATGAAATATTATACAATATTTGCAACAATGC
 CCTAAGAATTGTTAAATTCATGGAGTTATTTGTGCAGAATGACTCCAGAGAGCTCTACTTTCTG
 TTTTTTACTTTTCATGATTGGCTGTCTTCCATTATTCTGGTCATTTATTGCTAGTGACACTGT
 GCCTGCTTCCAGTAGTCTCATTTTCCCTATTTTGCTAATTTGTTACTTTTTCTTGCTAATTTGG
 AAGATTAACCTCATTTTAAATAAATATGTCTAAGATTAAGAAAAAAAAAAAAAAAAAAAAAAAAA
 AA

[illegible]

Important features:

amino acids 1-21

amino acids 195-199, 217-221, 272-276

amino acids 220-228

amino acids 120-126, 253-259, 268-274, 270-274, 285-291, 289-295

amino acids 267-271

amino acids 299-303

amino acids 127-169

amino acids 101-119

FIGURE 19

AATTCAGATTTTAAGCCCATTCTGCAGTGGAAATTCATGAACTAGCAAGAGGACACCATCTTCTT
GTATTATACAAGAAAGGAGTGACCTATCACACACAGGGGAAAAATGCTCTTTTGGGTGCTAGG
CCTCCTAATCCTCTGTGGTTTTCTGTGGACTCGTAAAGGAAAACATAAGATTGAAGACATCACTG
ATAAGTACATTTTATCACTGGATGTGACTCGGGCTTTGGAACTTGGCAGCCAGAATTTTGAT
AAAAAGGGATTTTCATGTAATCGCTGCCTGTCTGACTGAATCAGGATCAACAGCTTTAAAGGCAGA
AACCTCAGAGAGACTTCGTACTGTGCTTCTGGATGTGACCGACCCAGAGAATGTCAAGAGGACTG
CCCAGTGGGTGAAGAACCAAGTTGGGGAGAAAGGTCTCTGGGGTCTGATCAATAATGCTGGTGTT
CCCGCGTGCTGGCTCCCACTGACTGGCTGACACTAGAGGACTACAGAGAACCTATTGAAGTGAA
CCTGTTTGGACTCATCAGTGTGACACTAAATATGCTTCCTTTGGTCAAGAAAGCTCAAGGGAGAG
TTATTAATGTCTCCAGTGTTGGAGGTCGCCTTGCAATCGTTGGAGGGGGCTATACTCCATCCAAA
TATGCAGTGAAGGTTTCAATGACAGCTTAAGACGGGACATGAAAGCTTTTGGTGTGCACGTCTC
ATGCATTGAACCAGGATTGTTCAAAACAACTTGGCAGATCCAGTAAAGTAATTGAAAAAAAC
TCGCCATTTGGGAGCAGCTGTCTCCAGACATCAACAACAATATGGAGAAGGTTACATTGAAAAA
AGTCTAGACAACTGAAAGGCAATAAATCCTATGTGAACATGGACCTCTCTCCGGTGGTAGAGTG
CATGGACCACGCTCTAACAAGTCTCTTCCCTAAGACTCATTATGCCGCTGGAAAAGATGCCAAAA
TTTTCTGGATACCTCTGTCTCACATGCCAGCAGCTTTGCAAGACTTTTTATTGTTGAAACAGAAA
GCAGAGCTGGCTAATCCCAAGGCAGTGTGACTCAGCTAACCACAAATGTCTCCTCCAGGCTATGA
AATTGGCCGATTTCAAGAACACATCTCCTTTTCAACCCCATTCCTTATCTGCTCCAACCTGGACT
CATTTAGATCGTGCTTATTTGGATTGCAAAAGGGAGTCCCACCATCGCTGGTGGTATCCCAGGGT
CCCTGCTCAAGTTTTCTTTGAAAAGGAGGGCTGGAATGGTACATCACATAGGCAAGTCCTGCCCT
GTATTTAGGCTTTGCCTGCTTGGTGTGATGTAAGGAAATTGAAAGACTTGCCCATTCAAAATGA
TCTTTACCGTGGCTGCCCCATGCTTATGGTCCCCAGCATTTACAGTAACCTGTGAATGTTAAGT
ATCATCTCTTATCTAAATATTAAAAGATAAGTCAACCCAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAA

FIGURE 20

MLFWVLGLLILCGFLWTRKGKLIKIEDITDKYIFITGCDSGFGNLAARTFDKKGFHVIAACLTESG
STALKAETSERLRTVLLDVTDPENVKRTAQWVKNQVGEKGLWGLINNAGVPGVLAPTDLWTLEDY
REPIEVNLFGLISVTLNMLPLVKKAQGRVINVSSVGGRLAIVGGGYTPSKYAVEGFNDLRRDMK
AFGVHVSCEIEPGLFKNLADPVKVEKKLAIWEQLSPDIKQQYGEGYIEKSLDKLKGKNSYVNMD
LSPVVECDHALTSLFPKTHYAAGKDAKIFWIPLSHMPAALQDFLLLKQKAELANPKAV

Important features of the protein:

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 136-152

N-glycosylation sites.

amino acids 161-163, 187-190 and 253-256

Glycosaminoglycan attachment site.

amino acids 39-42

N-myristoylation sites.

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212

FIGURE 21

CTGAGGCGGCGGTAGCAATGGAGGGGGAGAGTACGTCGGCGGTGCTCTCGGGCTTTGTGCTCGGCG
 CACTCGCTTTCCAGCACCTCAACACGGACTCGGACACGGAAGGTTTTCTTCTTGGGGAAGTAAAA
 GGTGAAGCCAAGAACAGCATTACTGATTCCCAAATGGATGATGTTGAAGTTGTTTATACAATTGA
 CATTAGAAATATATTCCATGCTATCAGCTTTTGTAGCTTTTATAATTCTTCAGGCGAAGTAAATG
 AGCAAGCACTGAAGAAAATATTATCAAATGTCAAAAAGAATGTGGTAGGTTGGTACAAATTCCGT
 CGTCATTAGATCAGATCATGACGTTTAGAGAGAGGCTGCTTCACAAAACCTTGCAGGAGCATT
 TTCAAACCAAGACCTTGTTTTTCTGCTATTAACACCAAGTATAATAACAGAAAGCTGCTCTACTC
 ATCGACTGGAACATTCTTTATATAAACCTCAAAAAGGACTTTTTTCACAGGTTACCTTTAGTGTT
 GCCAATCTGGGCATGTCTGAACAACCTGGGTTATAAACTGTATCAGGTTCTGTATGTCCACTGG
 TTTTAGCCGAGCAGTACAAACACACAGCTCTAAATTTTTTGAAGAAGATGGATCCTTAAAGGAGG
 TACATAAGATAAATGAAATGTATGCTTCATTACAAGAGGAATTAAAGAGTATATGCAAAAAGTG
 GAAGACAGTGAACAAGCAGTAGATAAACTAGTAAAGGATGTAAACAGATTAAAACGAGAAATTGA
 GAAAAGGAGAGGAGCACAGATTAGGCGAGCAAGAGAGAAGAACATCCAAAAGACCTCAGGAGA
 ACATTTTTCTTTGTGAGGCATTACGGACCTTTTTTCCAAATCTGAATTTCTTCATTATGTGTT
 ATGTCTTTAAAAATAGACATGTTCTAAAAGTAGCTGTAACACACCACATCTCGATGTAGT
 AGACAATCTGACCTTAATGGTAGAACACACTGACATTCTGAAGCTAGTCCAGCTAGTACACCAC
 AAATCATTAAGCATAAAGCCTTAGACTTAGATGACAGATGGCAATTCAAGAGATCTCGGTTGTTA
 GATACACAAGACAAACGATCTAAAGCAAATACTGGTAGTAGTAACCAAGATAAAGCATCCAAAT
 GAGCAGCCCAGAAACAGATGAAGAAATTGAAAAGATGAAGGGTTTTGGTGAATATTCACGGTCTC
 CTACATTTTGATCTTTTTAACCTTACAAGGAGATTTTTTTATTTGGCTGATGGGTAAAGCCAAAC
 ATTTCTATTGTTTTTACTATGTTGAGCTACTTGCAGTAAGTTCATTTGTTTTTACTATGTTTACC
 TGTTTGAGTAATACACAGATAACTCTTAGTGCATTTACTTCACAAAGTACTTTTTCAACATCA
 GATGCTTTTATTTCCAAACCTTTTTTTCACCTTCACTAAGTTGTTGAGGGGAAGGCTTACACAG
 ACACATTCTTTAGAATTGGAAGAGTGAGACCAGGCACAGTGGCTCACACCTGTAATCCCAGCACT
 TAGGGAAGACAAGTCAGGAGGATTGATTGAAGCTAGGAGTTAGAGACCAGCCTGGGCAACGTATT
 GAGACCATGTCTATTAAAAAATAAAATGGAAGCAAGAATAGCCTTATTTTCAAAATATGGAAG
 GAAATTTATATGAAATTTATCTGAGTCATTAAATTTCTCCTTAAGTGATACTTTTTTAGAAGTA
 CATTATGGCTAGAGTTGCCAGATAAAATGCTGGATATCATGCAATAAATTTGCAAAACATCATCT
 AAAATTTAAAAAAAAAAAAAAAAAAAAA

Handwritten musical notation on a single staff.

Important features:

amino acids 1-19

amino acids 75-79, 322-326

amino acids 184-154

amino acids 134-150

FIGURE 24

MARFGLPALLCTLAVLSAALLAAELKSKSCSEVRRLYVSKGFNKNDAPLHEINGDHLKICPQGST
CCSQEMEKEYSLQSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAEKSLNDMFVKTYGH
LYMQNSELFKDLFVELKRYVVGNNLEMLNDFWARLLERMFRVNSQYHFTDEYLECVSKYTE
QLKPFQDVPRKLKLQVTRAFVAARTFAQGLAVAGDVVSKVSVVNPTAQCTHALLKMIYCSHCRGL
VTVKPCYNYCSNIMRGCLANQGDLD FEWNNFIDAMLMVAERLEGFFNIESVMDPIDVKISDAIMN
MQDNSVQVSQKVFQCGGPPKPLPAGRISRSISESAFSARFRPHHPEERPTTAAGTSLDRLVTDVK
EKLKQAKKFWSSLP SNVCNDEMAAGNGNEDDCWNGKGKSRYLEAVTGNGLANQGNNPEVQVDT
KPDILILRQIMALRVMTSKMKNAYNGNDVDFDISDESSGEGSGSGCEYQQCFSEFDYNATDHAG
KSANEKADSAGVRPGAQAYLLTVFCILFLVMQREWR

Important features:

Signal peptide:

amino acids 1-22

ATP/GTP-binding site motif A (P-loop).

amino acids 515-524

N-glycosylation site.

amino acids 514-518

Glycosaminoglycan attachment sites.

amino acids 494-498, 498-502

N-myristoylation sites.

amino acids 63-69, 224-230, 276-282, 438-444, 497-503, 531-537

Glypicans proteins.

amino acids 54-75, 105-157, 238-280, 309-346, 423-460, 468-506

FIGURE 25

CTCGCCCTCAAATGGGAACGCTGGCCTGGGACTAAAGCATAGACCACCAGGCTGAGTATCCTGAC
CTGAGTCATCCCCAGGGATCAGGAGCCTCCAGCAGGGAACCTTCCATTATATCTTCAAGCAACT
TACAGCTGCACCGACAGTTGCGATGAAAGTTCTAATCTCTTCCCTCCTCCTGTTGCTGCCACTAA
TGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGGTCGCCAGAGGCCACAGGGACCGAGGC
CAGGCTTCTAGGAGATGGCTCCAGGAAGGCGGCCAAGAATGTGAGTGCAAAGATTGGTTCCTGAG
AGCCCCGAGAAGAAAATTTCATGACAGTGTCTGGGCTGCCAAAGAAGCAGTGCCCCGTGTGATCATT
TCAAGGGCAATGTGAAGAAAACAAGACACCAAAGGCACCACAGAAAGCCAAACAAGCATTCCAGA
GCCTGCCAGCAATTTCTCAAACAATGTCAGCTAAGAAGCTTTGCTCTGCCTTTGTAGGAGCTCTG
AGCGCCCACTCTTCCAATTAAACATTCTCAGCCAAGAAGACAGTGAGCACACCTACCAGACACTC
TTCTTCTCCCACCTCACTCTCCCCTGTACCCACCCCTAAATCATTCCAGTGCTCTCAAAAAGCA
TGTTTTTCAAGATCATTTTGTGTTGTGCTCTCTAGTGTCTTCTTCTCTCGTCAGTCTTAGCCT
GTGCCCTCCCCTTACCCAGGCTTAGGCTTAATTACCTGAAAGATTCCAGGAACTGTAGCTTCCT
AGCTAGTGTCAATTTAACCTTAAATGCAATCAGGAAAGTAGCAAACAGAAGTCAATAAATATTTTT
AAATGTCAAAAAAAAAAAAAAAAAA

FIGURE 26

MKVLISLLLLLLPLMLMSMVSSSLNPGVARGHRDRGQASRRWLQEGGQECECKDWFLRAPRRKFM
TVSGLPKKQCPCDHFKGNVKKTRHQRHHRKPNKHSRACQQFLKQCQLRSFALPL

Important features:

Signal peptide:

amino acids 1-22

N-myristoylation sites.

amino acids 27-33, 46-52

.....

FIGURE 28

MDILVPLLQLLVLLLTLPPLHMLLGCWQPLCKSYFPYLMVLTPKSNRMESKKRELFSSQIKGL
 TGASGKVALLELGCGTGANFQFYPPGCRVTCLDPNPHFEKFLTKSMAENRHLQYERFVVAPGEDM
 RQLADGSMDVVVCTLVLCVQSPRKVLQEVRRVLRPGGVLFWEHVAEPYGSWAFMWQQVFEPTW
 KHIGDGCCLTRETWKDLENAQFSEIQMERQPPPLKWLPGPHIMGKAVKQSFSSKALICSFPSL
 QLEQATHQPIYLPLRGT

Important features:

Signal peptide:

amino acids 1-23

Leucine zipper pattern.

amino acids 10-32

N-myristoylation sites.

amino acids 64-70, 78-84, 80-86, 91-97, 201-207

FIGURE 29

CAATGTTTGCCTATCCACCTCCCCAAGCCCCTTTACCTATGCTGCTGCTAACGCTGCTGCTGCT
 GCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGGACTGGTCGGTGCCAGAAAGTCTCTTCTG
 CCACTGACGCCCCCATCAGGGATTGGGCCTTCTTTCCCCCTTCCTTTCTGTGTCTCCTGCCTCAT
 CGGCCTGCCATGACCTGCAGCCAAGCCCAGCCCCGTGGGGAAGGGGAGAAAGTGGGGGATGGCTA
AGAAAGCTGGGAGATAGGGAACAGAAGAGGGTAGTGGGTGGGCTAGGGGGGCTGCCTTATTTAAA
 GTGGTTGTTTATGATTCTTATACTAATTTATACAAAGATATTAAGGCCCTGTTCAATTAAGAAATT
 GTTCCCTTCCCCTGTGTTCAATGTTTGTAAGATTGTTCTGTGTAAATATGTCTTTATAATAAAC
 AGTTAAAAGCTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 30

MLLLTLLLLLLLLLKGSCLWGLVGAQKVSSATDAPIRDWAFPPSFLCLLPHRPAMTCSQAQPRG
EGEKVGDG

Important features:

Signal peptide:

amino acids 1-15

Growth factor and cytokines receptors family:

amino acids 3-18

FIGURE 31

GTTTGAATTCCTTCAACTATACCCACAGTCCAAAAGCAGACTCACTGTGTCCCAGGCTACCAAGTT
CCTCCAAGCAAGTCATTTCCCTTATTTAACCGATGTGTCCCTCAAACACCTGAGTGCTACTCCCT
ATTTGCATCTGTTTTGATAAATGATGTTGACACCCCTCCACCGAATTCTAAGTGGAATCATGTCGG
GAAGAGATAACAATCCTTGGCCTGTGTATCCTCGCATTAGCCTTGTCCTTTGGCCATGATGTTTACC
TTCAGATTCATCACCACCCTTCTGGTTCACATTTTCATTTCAATTGGTTATTTTGGGATTGTTGTT
TGTCTGCGGTGTTTTATGGTGGCTGTATTATGACTATACCAACGACCTCAGCATAGAATTGGACA
CAGAAAGGGAAAATATGAAGTGCGTGCTGGGGTTTGCTATCGTATCCACAGGCATCACGGCAGTG
CTGCTCGTCTTGATTTTTGTTCTCAGAAAGAGAATAAAATTGACAGTTGAGCTTTTCCAAATCAC
AAATAAAGCCATCAGCAGTGCTCCCTTCTGCTGTTCCAGCCACTGTGGACATTTGCCATCCTCA
TTTTCTTCTGGGTCTCTGGGTGGCTGTGCTGCTGAGCCTGGGAAGTGCAGGAGCTGCCCAGGTT
ATGGAAGGCGGCCAAGTGGAATATAAGCCCCCTTTCGGGCATTCCGGTACATGTGGTCGTACCATTT
AATTGGCCTCATCTGGACTAGTGAATTCATCCTTGCGTGCCAGCAAATGACTATAGCTGGGGCAG
TGGTTACTTGTTATTTCAACAGAAGTAAAAATGATCCTCCTGATCATCCCATCCTTTCTGCTCTC
TCCATTCTCTTCTTCTACCATCAAGGAACCGTTGTGAAAGGGTCATTTTTAATCTCTGTGGTGAG
GATTCCGAGAATCATTGTGATGTACATGCAAACGCACTGAAAGAACAGCAGCATGGTGCATTGT
CCAGGTACCTGTTCCGATGCTGCTACTGCTGTTTCTGGTGTCTTGACAAATACCTGCTCCATCTC
AACCAGAATGCATATACTACAACCTGCTATTAATGGGACAGATTTCTGTACATCAGCAAAAGATGC
ATTCAAAATCTTGTTCAAGAACTCAAGTCACCTTTACATCTATTAAGTCTTTGGAGACTTCATAA
TTTTTCTAGGAAAGGTGTTAGTGGTGTGTTTCACTGTTTTTGGAGGACTCATGGCTTTTAACTAC
AATCGGGCATTCCAGGTGTGGGCAGTCCCTCTGTTATTGGTAGCTTTTTTTGCCTACTTAGTAGC
CCATAGTTTTTTATCTGTGTTTGAACTGTGCTGGATGCACCTTTCTGTGTTTTGCTGTGATC
TGGAACAAAATGATGGATCGTCAGAAAAGCCCTACTTTATGGATCAAGAATTTCTGAGTTTCGTA
AAAAGGAGCAACAAATTAAACAATGCAAGGGCACAGCAGGACAAGCACTCATTAAAGGAATGAGGA
GGGAACAGAACTCCAGGCCATTGTGAGATAGATACCCATTTAGGTATCTGTACCTGGAAAACATT
TCCTTCTAAGAGCCATTTACAGAATAGAAGATGAGACCCTAGAGAAAAGTTAGTGAATTTTTTT
TAAAAAGACCTAATAAACCCCTATTCTTCCTCAAAA

$\frac{d}{dt} \left(\frac{\partial L}{\partial \dot{x}} \right) = \frac{\partial L}{\partial x}$

MSGRDTILGLCILALALSLAMMFTFRFITTLVHIFISLVILGLLFVCGVLWWLYDYDNDLSIE
LDTARENMKCVLGFAIVSTGITAVLLVLI FVLRKRIKLTVELFQITNKAISSAPFLLFQPLWTF
ILIFFWVLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFILACQOMTIA
GAVVTCYFNRSKNDPPDHPILSSLSILFFYHQGTVVKGSFLISVVRIPRIIVMYMQNALKEQQHG
ALSRYLFRCCYCCFWCLDKYLLHLNQNAYTTTAINGTDFCTSAKDAFKILSKNSSHFTSINCFGD
FIIFLGKVLVVCFTVFGGLMAFNYNRAQVWAVPLLLVAFFAYLVAHSFLSVFETVLDALFLCFA
VDLETNDGSSEKPYFMDOEFLSFVKRSNKLNNARAODKHSRLNEEGTELOAIVR

Important features:

Signal peptide:

amino acids 1-20

Putative transmembrane domains:

amino acids 35-54, 75-97, 126-146, 185-204, 333-350, 352-371

N-glycosylation sites.

amino acids 204-208, 295-299, 313-317

N-myristoylation sites.

amino acids 147-153, 178-184, 196-202, 296-275, 342-348

FIGURE 34

MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINCDVKAGKIIDPEFIVKCPAG
 CQDPKYHVGTDVYASYSSVCGAHVHSGVLDNSGGKILVRKVACQSGYKGSYNGVQSLSLPRWR
 ESFIVLESKPKKGVTPSALTYSSSKSPAAQAGETTKAYQRPPIPGTTAQPVTLMQLLAVTVAVA
 TPTTLPRPSPSAASTTSIPRPQSVGHRSEQEMDLWSTATYTSSQNRPRADPGIQRQDPSGAAFQKP
 VGADVSLGLVPKEELSTQSLEPVSLGDPNCKIDLSFLIDGSTSIGKRRFRIQKQLLADVAQALDI
 GPAGPLMGVVQYGDNPATHFNLKTHNTSRDLKTAIEKITQRGGLSNVGRAISFVTKNFFSKANGN
 RSGAPNVVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAAENEKQYVVEPNFANKAVCRTNG
 FYSLHVQSWFGLHKTLPVLRVCDTDRDLACSKTCLNSADIGFVIDGSSSVGTGNFRTVLQFVTN
 LTKEFEISDTRIGAVQYTYEQRLEFGFDKYSSKPDILNAIKRVGYWGGTSTGAAINFALEQL
 FKSKPNKRKLMILITDGRSYDDVRIPAMAAHLKGVITYAIGVAWAAQEELEVIATHPARDSFF
 VDEFNLHQYVPRIIQNICTEFNSQPRN

Important features:

Signal peptide:

amino acids 1-26

Transmembrane domain:

amino acids 181-200

N-glycosylation sites.

amino acids 390-394, 520-524

N-myristoylation sites.

amino acids 23-29, 93-99, 115-121, 262-268, 367-373, 389-395,
 431-437, 466-472, 509-515, 570-576, 571-577, 575-581, 627-633

Amidation site.

amino acids 304-308

FIGURE 35

CCGAGCACAGGAGATTGCCTGCGTTTAGGAGGTGGCTGCGTTGTGGGAAAAGCTATCAAGGAAGAAATTGC
 CAAACCATGTCTTTTTCTGTTTTTCAGAGTAGTTTCAACAGATCTGAGTGTTTTAATTAAGCATGGAAT
 ACAGAAAACAACAAAAAATAAGCTTTAATTTTCATCTGGAATCCACAGTTTTCTTAGCTCCCTGGACCC
 GGTTGACCTGTTGGCTCTTCCCGCTGGCTGCTCTATCACGTGGTGCTCTCCGACTACTCACCCGAGTGTA
 AAGAACCTTCGGCTCGCGTGCTTCTGAGCTGCTGTGGATGGCCTCGGCTCTCTGGACTGTCTTCCGAGTA
 GGATGTCACTGAGATCCCTCAAATGGAGCCTCCTGCTGCTGTCACTCCTGAGTTCTTTGTGATGTGGTAC
 CTCAGCCTTCCCACTACAATGTGATAGAACGCGTGAAGTGGATGTACTTCTATGAGTATGAGCCGATTTA
 CAGACAAGACTTTCACTTCACACTTCGAGAGCATTCAAAGTCTCTCATCAAAATCCATTTCTGGTCATTCT
 TGGTGACCTCCCACTTCAGATGTGAAAGCCAGGCAGGCCATTAGAGTTACTTGGGGTGAAAAAAGTCT
 TGGTGGGGATATGAGGTTCTTACATTTTTCTTATTAGGCCAAGAGGCTGAAAAGGAAGACAAATGTTGGC
 ATTTGTCCTTAGAGGATGAACACCTTCTTTATGGTGACATAATCCGACAAGATTTTTAGACACATATAATA
 ACCTGACCTTGAAACCATTTATGGCATTGAGGTGGGTAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT
 AAGACAGACACTGATGTTTTTCATCAATACTGGCAATTTAGTGAAGTATCTTTTAAACCTAAACCACTCAGA
 GAAGTTTTTCACAGGTTATCCTCTAATTGATAATTATTCTATAGAGGATTTTACCAAAAAACCCATATTT
 CTTACCAGGAGTATCCTTTCAAGGTGTTCCCTCCATACTGCAGTGGGTGGGTATATAATGTCCAGAGAT
 TTGGTGCCAAAGGATCTATGAAATGATGGGTGACGTAACCCATCAAGTTTGAAGATGTTTATGTCGGGAT
 CTGTTTGAATTTATTAAGTGAACATTCATATTCCAGAAGACACAAATCTTTCTTTCTATATAGAATCC
 ATTTGGATGTCTGTCAACTGAGACGTGTGATTGCAGCCCATGGCTTTCTTCCAAGGAGATCATCACTTTT
 TGGCAGGTCATGCTAAGGAACACCACATGCCATTATTAACTTCACATTTCTACAAAAAGCCTAGAAGGACAG
 GATACCTTGTGAAAGTGTTAAATAAAGTAGGTACTGTGAAAATTCATGGGGAGGTGAGTGTCTGGCTT
 AACTGAACTGAACTCATGAAAACCCAGACTGGAGACTGGAGGGTTACACTTGTGATTTATTAGTCAGG
 CCCTTCAAAGATGATATGTGGAGGAATTAATATAAAGGAATTGGAGGTTTTTGCTAAAGAAATTAATAGG
 ACCAAACAATTTGGACATGTCATTCTGTAGACTAGAATTTCTTAAAGGGTGTACTGAGTTATAAGCTCA
 CTAGGCTGTAAAAACAAAACAATGTAGAGTTTATTATTGAACAATGTAGTCACTTGAAGGTTTTGTGTA
 TATCTTATGTGGATTACCAATTTAAAAATATATGTAGTTCTGTGTCAAAAACTTCTTCACTGAAGTTATA
 CTGAACAAAATTTTACCTGTTTTGGTCATTATAAAGTACTTCAAGATGTTGCAGTATTTACAGTTATT
 ATTATTTAAATTAATTCACTTTGTTGTTTTAAATGTTTTGACGATTTCAATACAAGATAAAAAGGATAG
 TGAATCATTTCTTACATGCAACATTTCCAGTTACTTAACTGATCAGTTTATTATTGATACATCACTCCA
 TTAATGTAAAGTCATAGGTCATTATTGCATATCAGTAATCTCTGGACTTTGTTAAATATTTACTGTGGT
 AATATAGAGAAGAATTAAGCAAGAAAATCTGAAA

FIGURE 36

MASALWTVLPSRMSLRSLKWSLLLLSLLSFFVMWYLSLPHYNVIERVNWMYFYEYEPYRQDFHF
 TLREHSNCSHQNPFLVILVTSHPSDVKARQAIRVTWGEKKSWWGYEVLTFLLGQEA EKEDKMLA
 LSLEDEHLLYGDIIRQDFLDTYNNLT LKTIMAFRWVTEFCPNAKYVMKTD TDVFINTGNLVKYL
 NLNHSEKFFTGYPLIDNYSYRGFYQKTHISYQEYPFKVFPYCSGLGYIMSRDLVPRIYEMMGHV
 KPIKFEDVYVGICLNLLKVNIIHIPEDTNLFFLYRIHLDVCQLRRVIAAHGFSKEIITFWQVMLR
 NTTCHY

Important features:

Type II transmembrane domain:

amino acids 20-39

N-glycosylation sites.

amino acids 72-76, 154-158, 198-202, 212-216, 326-330

Glycosaminoglycan attachment site.

amino acids 239-243

Ly-6 / u-PAR domain proteins.

amino acids 23-37

N-myristoylation site.

amino acids 271-277

FIGURE 37

CGCTCGGGCACCAGCCGCGGCAAGGATGAGCTGGGTTGCTGGACGAGTTGGGGCTCACTTTTCTTCAGCTCCTTCTCATC
TCGTCTTGGCAAGAGAGTACACAGTCATTATGAAGCCTGCCCTGGAGCAGAGTGAATATCATGTGTCGGGAGTGCTGTG
AATATGATCAGATTGAGTGCCTCTGCCCCGAAAGAGGGAAGTCGTGGTTATACCATCCCTTGCTGCAGGAATGAGGAGAA
TGAGTGTGACTCCTGCCTGATCCACCCAGTTGTACCATCTTTGAAAACGCAAGAGCTGCCGAAATGGCTCATGGGGGGGT
ACCTTGGATGACTTCTATGTGAAGGGTTCTACTGTGCAGAGTGCCGAGCAGGCTGGTACGGAGGAGACTGCATGCGATGTG
GCCAGGTTCTGCAGAGCCCCAAAGGGTCAGATTTTGTGGAAAGCTATCCCTTAAATGCTCACTGTGAATGGACCATTTCATGC
TAAACCTGGGTTTGTTCATCCAATAAGATTGTTCATGTTGAGTCTGGAGTTTGACTACATGTGCCAGTATGACTATGTTGAG
GTTCTGTGATGGAGACAACCGCATGGCCAGATCATCAAGCGTGTCTGTGGCAACGAGCGGCCAGCTCCTATCCAGAGCATAG
GATCTCACTCCACGTCCTCTTCCACTCCGATGGCTCCAAGAATTTTGACGGTTTCATGCCATTTATGAGGAGATCACAGC
ATGCTCCTCATCCCCCTGTTCATGACGGCAGTGCCTCTTGACAAGGCTGGATCTTACAAGTGTGCTGCTTGGCAGGC
TATACGGGAGCGCTGTGAAAATCTCCTTGAAGAAAGAACTGCTCAGACCTGGGGGCCAGTCAATGGGTACCAAGAAA
TAACAGGGGGCCCTGGGCTTATCAACGGAGCCCATGCTAAAATTGGCACCCTGGTGTCTTTCTTTTGAACAACTCCTATGT
TCTTAGTGGCAATGAGAAAAGAACTTGCCAGCAGAATGGAGAGTGGTCAGGGAACAGCCCATCTGCATAAAAGCCTGCCGA
GAACCAAGATTTCAGACCTGGTGAGAAGGAGAGTTCTTCCGATGCAAGTTTCAGTCAAGGGAGACACCATACACAGCTAT
ACTCAGCGGCCCTTCAGCAAGCAGAACTGCAGAGTGCCTTACCAAGAAGCCAGCCCTTCCCTTTGGAGATCTGCCATGGG
ATACCAACATCTGCATACCCAGTCCAGTATGAGTGCATCTCACCCTTCTACCGCCGCTGGGCAGCAGCAGGAGCATGT
CTGAGGACTGGGAAGTGGAGTGGGCGGGCACCATCCTGCATCCCTATCTGCGGGAAAATTGAGAACATCACTGCTCCAAAGA
CCCAAGGGTTGCGCTGGCGTGGCAGGCAGCCATCTACAGGAGGACCAGCGGGTGCATGACGGCAGCCTACACAAGGGAGC
GTGGTTCTTAGTCTGCAGCGGTGCCCTGGTGAATGAGCGCACTGTGGTGGTGGCTGCCCATGTGTTACTGACCTGGGGAAG
GTCACCATGATCAAGACAGCAGACCTGAAGTTGTTTGGGGAAAATTCTACCGGGATGATGACCGGATGAGAAGACCATCC
AGAGCCTACAGATTTCTGCTATCATCTGCATCCAACTATGACCCCATCTGCTGTGATGCTGACATCGCCATCCTGAAGCT
CCTAGACAAGGCCCGTATCAGCACCAGTCCAGCCCATCTGCCTCGCTGCCAGTGGGATCTCAGCACTTCCTTCCAGGAG
TCCCACATCACTGTGGCTGGCTGGAATGTCTTGGCAGAGTGAAGAGCCCTGGCTTCAAGAACGACACACTGCGCTCTGGGG
TGGTCAGTGTGGTGGACTCGCTGCTGTGTGAGGAGCAGCATGAGGACCATGGCATCCCAGTGAAGTGTCACTGATAACATGTT
CTGTGCCAGCTGGGAACCCACTGCCCTTCTGATATCTGCATGCAAGAGACAGGAGCATCGCGGCTGTGTCCTTCCCGGGA
CGAGCATCTCCTGAGCCACGCTGGCATCTGATGGGACTGGTCAGCTGGAGCTATGATAAAACATGCAGCCACAGGCTCTCCA
CTGCCCTTACCAAGGTGCTGCCCTTTAAAGACTGGATGAAAGAAATATGAAATGAACCATGCTCATGCACTCCTTGAGAAG
TGTTTCTGTATATCCGTCTGTACGTGTGTCATTGCGTGAAGCAGTGTGGCCTGAAGTGTGATTGGCCTGTGAAGTGTGGCT
GTGCCAGGGCTTCTGACTTCAGGGACAAAACCTAGTGAAGGGTGAGTAGACCTCCATTGCTGGTAGGCTGATGCCGCTCCA
CTACTAGGACAGCCAATTGGAAGATGCCAGGGCTTGCAAGAAGTAAGTTTCTTCAAAGAAGACCATATACAAAACCTCTCCA
CTCCACTGACCTGGTGGTCTTCCCCAACTTTCAGTTATACGAATGCCATCAGCTTGACCAGGGAAGATCTGGGCTTCATGAG
GCCCCCTTTGAGGCTCTCAAGTCTAGAGAGCTGCCTGTGGGACAGCCAGGGCAGCAGAGCTGGGATGTGGTGCATGCGCTT
TGTGTACATGGCCACAGTACAGTCTGGTCTTTTCTTCCCATCTCTTGTACACATTTAATAAAATAAGGGTTGGCTTCT
GAACTACAAAAA
AAAAA

FIGURE 38

MELGCWTQLGLTFLQLLLISSLPREYTVINEACPGAENIMCRECCEYDQIECVCPGKREVVGYT
 IPCCRNEENECDSCLIHPGCTIFENCKSCRNGSWGGLDDFYVKGIFYCAECRAGWYGGDCMRGQ
 VLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRDGDNRDQII
 KRVCGNERPAPIQSIGSSLHVLHSDGSKNFDGFHAIYEEITACSSSPCFHDGTCVLDKAGSYKC
 ACLAGYTGQRCENLLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGTVVSFFCNNSYVLSGNE
 KRTCQQNGEWSGKQPICIKACREPKISDLVRRRVLPQVQSRETPLHQLYSAAFSKQKLSAPTK
 KPALPFGDLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPSCIPICGKIENITAP
 KTQGLRWPWQAAIYRRTSGVHDGSLHKGAWFLVCSGALVNERTVVVAHCVTDLGKVTMIKTADL
 KVVLGKFYRDDDRDEKTIQSLQISAILHPNYDPILLDADIAILKLLDKARISTRVQPICLAASR
 DLSTSFQESHITVAGWNVLADVRSPGFKNDFLRSGVSVVDSLLCEEQHEDHGIPVSVTDNMFCA
 SWEPTAPSDICTAETGGIAAVSFPGRASPEPRWHLMLVSWSYDKTCSHRLSTAFTKVLFPKDWI
 ERNMK

Important features of the protein:**Signal peptide:**

amino acids 1-23

EGF-like domain cysteine pattern signature.

amino acids 260-272

N-glycosylation sites.

amino acids 96-100, 279-283, 316-320, 451-455, 614-618

N-myristoylation sites.amino acids 35-41, 97-103, 256-262, 284-290, 298-304, 308-314,
474-480, 491-497, 638-644, 666-672**Amidation site.**

amino acids 56-60

Serine proteases, trypsin family.

amino acids 489-506

CUB domain proteins profile.

amino acids 150-167

FIGURE 39

GGTTCCTACATCCTCTCATCTGAGAATCAGAGAGCATAATCTTCTTACGGGCCCGTGATTTATTAACGTGGCTTAATC
TGAAGGTTCTCAGTCAAATTCCTTGTGATCTACTGATTGTGGGGCATGGCAAGGTTTGCTTAAAGGAGCTTGGCTGG
TTTGGGCCCTTTAGCTGACAGAAGGTGGCCAGGGAGAATGCAGCACACTGCTCGGAGAATGAAGGCGCTTCTGTGTC
TGGTCTTGCCCTTGGCTCAGTCTGCTAACTACATTGACAATGTGGGCAACCTGCACCTTCTGTATTCAGAACTCTGTA
AAGGTGCCTCCCACTACGGCTGACCAAGATAGGAAGAGGCGCTCACAAGATGGCTGTCCAGACGGCTGTGCCAGCC
TCACAGCCACGGCTCCCTCCCAAGAGGTTTCTGCAGCTGCCACCATCTCTTAATGACAGACGAGCTTGGCTTAGACA
ACCTTGCTTACGTGTCTCGGCAGAGGACGGGCAGCCAGCAATCAGCCAGTGGACTCTGGCCGGAGCAACCGAACTA
GGGCACGGCCCTTTGAGAGATCCACTATTAGAAGCAGATCATTTAAAAAAATAAATCGAGCTTTGAGTGTCTTCGAA
GGACAAAGAGCGGGAGTGCAGTTGCCAACCATGCCAGGCGAGGGAAAAATCTGAAAACACCACTGCCCTGAAG
TCTTTCCAAGGTTGTACACCTGATTCCAGATGGTGAATTAACAGCATCAAGATCAATCGAGTAGATCCCAAGTGA
GCCTCTCTATTAGGCTGGTGGAGGTAGCGAAACCCCACTGGTCCATATCATTTATCCAACACATTTATCGTGATGGGG
TGATCGCCAGAGACGGCCGGCTACTGCCAGGAGACATCATTTAAAGGTCAACGGGATGGACATCAGCAATGTCCTC
ACAACTACGCTGTGCGTCTCTTGCAGGCGCCCTGCCAGGTGCTGTGGCTGACTGTGATGCGTGAACAGAAGTCCGCA
GCAGGAACAATGGACAGGCCCGGATGCCTACAGACCCCGAGATGACAGCTTTTCATGTGATTCTCAACAAAAGTAGCC
CCGAGGAGCAGCTTGAATAAACTGGTGCAGAGGTGGATGAGCCTGGGGTTTTCATCTTCAATGTGCTGGATGGCG
GTGTGGCATATCGACATGGTCAGCTTGAGGAGAATGACCGTGTGTAGCCATCAATGGACATGATCTTCGATATGGCA
GCCCAGAAAGTGGGCTCATCTGATTGAGGCCAGTGAAGACGTGTTACCTCGTGTGTCGCCAGGTTCCGGCAGC
GGAGCCCTGACATCTTTCAGGAAGCCGGCTGGAACAGCAATGGCAGCTGCTCCCAAGGCCAGGGGAGAGGAGCAACA
CTCCCAAGCCCTCCATCTACAATTAATGTGTCATGAGAAGGTGGTAAATATCCAAAAGACCCCGGTGAATCTCTCG
GCATGACCGTCGAGGGGAGCATCACATAGAGAATGGGATTGGCTATCTATGTCATCAGTGTGAGCCCGGAGGAG
TCATAAGCAGAGATGGAAGAATAAAACAGGTGACATTTTGTGAAATGTGGATGGGGTCGAACGACAGAGGTGAGCC
GGAGTGAGGCGAGTGGCATTATTGAAAAGAACATCATCTCGATAGTACTCAAAGCTTTGGAAGTCAAAGAGTATGAGC
CCCAGGAAGACTGCAGCAGCCAGCAGCCCTGGACTCCAACCACAACATGGCCCCACCCAGTGACTGGTCCCATCTCT
GGGTGATGTGGCTGGAATTACCACGGTGTGTATACTGTAAAGATATGTATTACGAAGAAACACAGCTGGAAGTCT
TGGGCTTCTGCATTGTAGGAGTTATGAAGAATACAATGGAACAAACCTTTTTCATCAAATCCATTGTTGAAGGAA
CACCAGCATACAATGATGGAAGAATTAGATGTGGTGATATTCTTCTGTGTCAATGGTAGAAGTACATCAGGAATGA
TACATGCTTGCTTGGCAAGACTGCTGAAAGAACTTAAAGGAAGAATTACTCTAACTATTGTTTCTTGGCCTGGCACTT
TTTTATGAATCAATGATGGGTCAGAGGAAAACAGAAAAATCACAAATAGGCTAAGAAGTTGAAACACTATATTTATC
TTGTGAGTTTTATATTTAAAGAAAGAAATACATTGTAAAAATGTGAGGAAAAGTATGATCATCTAATGAAAGCCAGTT
ACACCTCAGAAAATATGATCCAAAAAAATTAAGTACTAGTTTTTTTTTCAGTGTGGAGGATTCTCATTACTCTAC
AACATTGTTTATATTTTCTATTCAATAAAAAGCCCTAAACAACATAAATGATTGATTGTATATCCCACTGAATT
CAAGCTGATTTAAATTTAAATTTGGTATATGCTGAAGTCTGCCAAGGGTACATATGGCCATTTTAAATTTACAGCT
AAAAATTTTTTAAATGCATTGCTGAGAAACGTTGCTTTCATCAAACAAGAATAAATATTTTTTCAAGAGTTAA

FIGURE 40

MKALLLLVLPWLSPANYIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGCPCDGCASLTATAPS
 PEVSAAATISLMTDEPGLDNPAYVSSAEDGQPAISPVDSGRSNRTRARPFERSTIRSRSEFKKINR
 ALSVLRRTKSGSAVANHADQGRESENTTAPAEVFPRLYHLIPDGEITSIKINRVPSESLSIRLV
 GGSETPLVHIIIQHIYRDGVIARDGRLLPGDIILKVNGMDISNVPHNYAVRLLRQPCQVLWLTVM
 REQKFRSRNNGQAPDAYRPRDDS FHVILNKSSPEEQLGIKLVRKVDEPGVFIFNVLDGGVAYRHG
 QLEENDRVLAINGHDLRYGSPESAHLIQASERRVHLVVSQRQVRQSPDIFQEAGWNSNGSWSPG
 PGRSNTPKPLHPTITCHEKVNIQKDPGESLGMTVAGGASHREWDLPIYVISVEPGGVISRDR
 IKTGDILLNVGVELTEVSRSEAVALLKRTSSSIVLKALEVKEYEPQEDCSSPAALDSNHNMAP
 SDWSPSWVMWLELPRCLYNCKDIVLRRNTAGSLGFCIVGGYEEYNGNKPFFIKSIVEGTPAYNDG
 RIRCGDILLAVNGRSTSGMIHACLARLLKELKGRITLTIVSWPGTFL

Important features:

Signal peptide:

amino acids 1-15

N-glycosylation sites.

amino acids 108-112, 157-161, 289-293, 384-388

Tyrosine kinase phosphorylation sites.

amino acids 433-441, 492-500

N-myristoylation sites.

amino acids 51-57, 141-147, 233-239, 344-350, 423-429, 447-453,
 467-473, 603-609

FIGURE 41

ACCAGGCATTGTATCTTCAGTTGTCATCAAGTTCGCAATCAGATTGGAAAAGCTCAACTTGAAGCTTT
 CTTGCCTGCAGTGAAGCAGAGAGATAGATATTATTACGTAATAAAAAACATGGGCTTCAACCTGACT
 TTCCACCTTTCTTACAAATTCCGATTACTGTTGCTGTTGACTTTGTGCCTGACAGTGGTTGGGTGGGC
 CACCAGTAACACTTCTGTGGGTGCCATTCAAGAGATTCTTAAAGCAAAGGAGTTCATGGCTAATTTCC
 ATAAGACCCTCATTTTGGGGAAGGGAAAACTCTGACTAATGAAGCATCCACGAAGAAGGTAGAACTT
 GACAACTGTCTTCTGTGTCTCCTTACCTCAGAGGCCAGAGCAAGCTCATTTTCAAACCAGATCTCAC
 TTTGGAAGAGGTACAGGCAGAAAATCCCAAAGTGTCCAGAGGCCGGTATCGCCCTCAGGAATGTAAAG
 CTTTACAGAGGGTCGCCATCCTCGTTCCCCACCGAACAGAGAGAAACACCTGATGTACCTGCTGGAA
 CATCTGCATCCCTTCCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTCATCCACCAGGCTGAAGG
 TAAAAAGTTTAAATCGAGCCAAACTCTTGAATGTGGGCTATCTAGAAGCCCTCAAGGAAGAAAATTGGG
 ACTGCTTTTATATTCCACGATGTGGACCTGGTACCCGAGAATGACTTTAACCTTTACAAGTGTGAGGAG
 CATCCCAAGCATCTGGTGGTTGGCAGGAACAGCACTGGGTACAGGTTACGTTACAGTGGATATTTTGG
 GGGTGTACTGCCCTAAGCAGAGAGCAGTTTTTCAAGGTGAATGGATTCTCTAACAACACTACTGGGGAT
 GGGGAGGCGAAGACGATGACCTCAGACTCAGGGTTGAGCTCCAAAGAATGAAAATTTCCCGGCCCTG
 CCTGAAGTGGGTAAATATACAATGGTCTTCCACACTAGAGACAAAGGCAATGAGGTGAACGCAGAACG
 GATGAAGCTCTTACACCAAGTGTACGAGTCTGGAGAACAGATGGGTTGAGTAGTTGTCTTTATAAAT
 TAGTATCTGTGGAACACAATCCTTTATATATCAACATCACAGTGGATTTCTGGTTTGGTGCATGACCC
 TGGATCTTTTGGTGATGTTTGAAGAACGATTCCTTTGTTTGAATAATTTTGGCCTAGAGACTTCAA
 ATAGTAGCACACATTAAGAACCTGTTACAGCTCATTGTTGAGCTGAATTTTTCCTTTTTGTATTTCT
 TAGCAGAGCTCCTGGTGATGTAGAGTATAAAACAGTTGTAACAAGACAGCTTCTTAGTCATTTTGAT
 CATGAGGGTTAAATATTGTAATATGGATACTTGAAGGACTTTATATAAAAGGATGACTCAAAGGATAA
 AATGAACGCTATTTGAGGACTCTGGTTGAAGGAGATTTATTTAAATTTGAAGTAATATATATGGGAT
 AAAAGGCCACAGGAAATAAGACTGCTGAATGTCTGAGAGAACCAGAGTTGTTCTCGTCCAAGGTAGAA
 AGGTACGAAGATACAATACTGTTATTCATTTATCCTGTACAATCATCTGTGAAGTGGTGGTGTGAGGT
 GAGAAGGCGTCCACAAAAGAGGGGAGAAAAGGCGACGAATCAGGACACAGTGAACCTGGGAATGAAGA
 GGTAGCAGGAGGGTGGAGTGTGGCTGCAAAGGCAGCAGTAGCTGAGCTGGTTGCAGGTGCTGATAGC
 CTTACAGGGGAGGACCTGCCCAGGTATGCCCTCCAGTGATGCCACCAGAGAATACATTCTCTATTAGT
 TTTTAAAGAGTTTTTGTAAAATGATTTGTACAAGTAGGATATGAATTAGCAGTTTACAAGTTTACAT
 ATTAATAATAATAATATGTCTATCAAATACCTCTGTAGTAAAATGTGAAAAAGCAAAA

FIGURE 42

MGFNLT FHLSYKFRLLLLLTLCLTVVGWATSNYFVGAIQEIPKAKEFMANFHKTLILGKGKTLTN
EASTKKVELDNCPSVSPYLRGQSKLIFKPDLTLEEVQAENPKVSRGRYRPQECKALQRVAILVPH
RNREKHLMYLLEHLHPFLQRQQLDYGIYVIHQAEKGKFNRAKLLNVGYLEALKEENWDCFI FHDV
DLVPENDFNLYKCEEHPKHLVVGRNSTGYRLRYSGYFGGV TALSREQFFKVNGFSNNYWGWGGE
DDLRLRVELQRMKISRPLPEVGKYTMVFHTRDKGNEVNAERMKLLHQVSRVWRDGLSSCSYKLV
SVEHNPLYINITVDFWFGA

Important features:

Signal peptide:

amino acids 1-27

N-glycosylation sites.

amino acids 4-8, 220-224, 335-339

Xylose isomerase proteins.

amino acids 191-202

FIGURE 43

GCTCAAGACCCAGCAGTGGGACAGCCAGACAGACGGCACGATGGCACTGAGCTCCCAGATCTGGG
 CCGCTTGCCTCCTGCTCCTCCTCCTCGCCAGCCTGACCAGTGGCTCTGTTTTCCCAACAG
 ACGGGACAACCTGCAGAGCTGCAACCCAGGACAGAGCTGGAGCCAGGGCCAGCTGGATGCCCAT
 GTTCCAGAGGCGAAGGAGGCGAGACACCCACTTCCCCATCTGCATTTTCTGCTGCGGCTGCTGTC
 ATCGATCAAAGTGTGGGATGTGCTGCAAGACGTAGAACCTACCTGCCCTGCCCCGTCCTCCCTCCC
 TTCCTTATTTATTCCTGCTGCCCCAGAACATAGGTCTTGGAATAAAATGGCTGGTTCTTTTGTTT
 TCCAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 44

MALSSQIWAACLLLLLLLLSLTSGSVFPQQTGQLAELQPQDRAGARASWMPMFQRRRRRDTHFPI
CIFCCGCCHRSKCGMCCKT

Important features:

Signal peptide:

amino acids 1-24

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 58-59

N-myristoylation site.

amino acids 44-50

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 1-12

FIGURE 45

GTGGCTTCATTTTCAGTGGCTGACTTCCAGAGAGCAATATGGCTGGTTCCCCAACATGCCTCACCC
TCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAAGAGCTGGTCGGT
TCCGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTCCAAAGTAAAGCAAGTTGACTCTATTGTCTG
GACCTTCAACACAACCCCTCTTGTCACCATAACAGCCAGAAGGGGGCACTATCATAGTGACCCAAA
ATCGTAATAGGGAGAGAGTAGACTTCCCAGATGGAGGCTACTCCCTGAAGCTCAGCAAAGTGAAG
AAGAATGACTCAGGGATCTACTATGTGGGGATATACAGCTCATCACTCCAGCAGCCCTCCACCCA
GGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGCAGAGCA
ATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATGGAACATGGGGAAGAGGATGTGATT
TATACCTGGAAGGCCCTGGGGCAAGCAGCCAATGAGTCCCATAATGGGTCCATCTCCCCATCTC
CTGGAGATGGGGAGAAAGTGATATGACCTTCATCTGCGTTGCCAGGAACCCGTGCAGCAGAAACT
TCTCAAGCCCCATCCTTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCTCCATG
GTCCTCCTGTGTCTCCTGTTGGTGCCCTCCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTG
GTTTCTGAAGAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTCGGG
AAACTCCTAACATATGCCCCATTCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAAT
AGAACAATCCTAAAGGAAGATCCAGCAAATACGGTTTACTCCACTGTGGAAATACCGAAAAAGAT
GGAAAATCCCCACTCACTGCTCACGATGCCAGACACACCAAGGCTATTTGCCTATGAGAATGTTA
TCTAGACAGCAGTGCACTCCCCTAAGTCTCTGCTCA

FIGURE 46

MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPLVTIQP
EGGTIIIVTQNRNRERVDFFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYVLHVYEHLSK
PKVTMGLQSNKNGTCVTNLTCCEHGEEDVIYTWKALGQAANESHNGSILPISWRWGESDMTFIC
VARNPVS RNFS PILARKLCEGAADDPDSSMVLLCLLLVPLLLSLFVLGLFLWFLKRERQEEYIE
EKKRVDICRETPNICPHSGENT EYDTIPHTNRTILKEDPANTVYSTVEIPKKMENPHSLLTMPDT
PRLFAYENV I

Important features:

Signal peptide:

amino acids 1-22

Transmembrane domain:

amino acids 224-250

Leucine zipper pattern.

amino acids 229-251

N-glycosylation sites.

amino acids 98-102, 142-146, 148-152, 172-176, 176-180, 204-208,
291-295

FIGURE 47

GGCTCGAGCGTTTCTGAGCCAGGGGTGACCATGACCTGCTGCGAAGGATGGACATCCTGCAATGG
 ATTCAGCCTGCTGGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATACCTCTAATTGTCAGCT
 TAGTTGAGGAAGACCAATTTTCTCAAACCCCATCTCTTGCTTTGAGTGGTGGTTCCCAGGAATT
 ATAGGAGCAGGTCTGATGGCCATTCCAGCAACAACAATGTCCTTGACAGCAAGAAAAAGAGCGTG
 CTGCAACAACAGAACTGGAATGTTTCTTTCATCATTTTTCAGTGTGATCACAGTCATTGGTGCTC
 TGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAGGTCCTCTCATGTGTAATTCCTCAAGC
 AACAGTAATGCCAATTGTGAATTTTCATTGAAAAACATCAGTGACATTCATCCAGAATCCTTCAA
 CTTGCAGTGGTTTTTCAATGACTCTTGTGCACCTCCTACTGGTTTCAATAAACCCACCAGTAACG
 ACACCATGGCGAGTGGCTGGAGAGCATCTAGTTTCCACTTCGATTCTGAAGAAAACAAACATAGG
 CTTATCCACTTCTCAGTATTTTATAGGTCTATTGCTTGTGGAATTCTGGAGGTCCTGTTTGGGCT
 CAGTCAGATAGTCATCGGTTTCCTTGGCTGTCTGTGTGGAGTCTCTAAGCGAAGAAGTCAAATTG
 TGTAGTTTAAATGGGAATAAAATGTAAGTATCAGTAGTTTGAAAAAAAAAAAA

FIGURE 48

MTCCEGWTSCNGFSLVLLVLLLVNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMAIPA
 TTMSLTARKKRACNNRTGMFLSSFFSVITVIGALYCLISIQALLKGPLMCNSPSNSNANCEFSL
 KNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHFSEENKHRLIHFSVFLGL
 LLVGILEVLFGLSQIVIGFLGCLCGVSKRRSQIV

Important features:

Transmembrane domains:

amino acids 10-31 (type II), 50-72, 87-110, 191-213

N-glycosylation sites.

amino acids 80-84, 132-136, 148-152, 163-167

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 223-227

N-myristoylation sites.

amino acids 22-28, 54-60, 83-89, 97-103, 216-222

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 207-218

TNFR/NGFR family cysteine-rich region protein.

amino acids 4-12

[illegible]

APP_ID=10063520

FIGURE 50

MERVTLALLLLAGLTALEANDPFANKDDPFYDWKNLQLSGLICGGLLAIAAGTAAVLSGKCKYKS
SQKQHSPVPEKAIPLITPGSATTC

Important features:

Signal peptide:

amino acids 1-16

Transmembrane domain:

amino acids 36-59

N-myristoylation sites.

amino acids 41-47, 45-51, 84-90

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7.

amino acids 54-67

FIGURE 51

GTGGACTCTGAGAAGCCCAGGCAGTTGAGGACAGGAGAGAGAAGGCTGCAGACCCAGAGGGAGGG
 AGGACAGGGAGTCGGAAGGAGGAGGACAGAGGAGGGCACAGAGACGCAGAGCAAGGGCGGCAAGG
 AGGAGACCCTGGTGGGAGGAAGACACTCTGGAGAGAGAGGGGGCTGGGCAGAGATGAAGTTCCAG
 GGGCCCTGGCCTGCCTCCTGCTGGCCCTCTGCCTGGGCAGTGGGGAGGCTGGCCCCCTGCAGAG
 CGGAGAGGAAAGCACTGGGACAAATATTGGGGAGGCCCTTGACATGGCCTGGGAGACGCCCTGA
 GCGAAGGGGTGGGAAAGGCCATTGGCAAAGAGGCCGGAGGGGCAGCTGGCTCTAAAGTCAGTGAG
 GCCCTTGGCCAAGGGACCAGAGAAGCAGTTGGCACTGGAGTCAGGCAGGTTCCAGGCTTTGGCGC
 AGCAGATGCTTTGGGCAACAGGGTCGGGGAAGCAGCCCATGCTCTGGGAAACTGGGCACGAGA
 TTGGCAGACAGGCAGAAGATGTCATTGACACGGAGCAGATGCTGTCCGGGCTCCTGGCAGGGG
 GTGCCCTGGCCACAGTGGTGCTTGGGAACTTCTGGAGGCCATGGCATCTTTGGCTCTCAAGGTGG
 CCTTGGAGGCCAGGGCCAGGGCAATCCTGGAGGTCTGGGGACTCCGTGGGTCCACGGATACCCCG
 GAAACTCAGCAGGCAGCTTTGGAATGAATCCTCAGGGAGCTCCCTGGGGTCAAGGAGGCAATGGA
 GGGCCACCAAACCTTTGGGACCAACACTCAGGGAGCTGTGGCCCAGCCTGGCTATGGTTTCAGTGAG
 AGCCAGCAACCAGAATGAAGGGTGACGAATCCCCACCATCTGGCTCAGGTGGAGGCTCCAGCA
 ACTCTGGGGGAGGCAGCGGCTCACAGTCGGGCAGCAGTGGCAGTGGCAGCAATGGTGACAACAAC
 AATGGCAGCAGCAGTGGTGGCAGCAGCAGTGGCAGCAGCAGTGGCAGCAGCAGTGGCGGCAGCAG
 TGGCGGCAGCAGTGGTGGCAGCAGTGGCAACAGTGGTGGCAGCAGAGGTGACAGCGGCAGTGAGT
 CCTCTGGGGATCCAGCACCGGCTCCTCCTCCGGCAACCACGGTGGGAGCGGCGGAGGAAATGGA
 CATAAACCCGGGTGTGAAAAGCCAGGGAATGAAGCCCGGGAGCGGGGAATCTGGGATTACAGG
 CTTTCAGAGGACAGGGAGTTTCCAGCAACATGAGGGAAATAAGCAAAGAGGGCAATCGCCTCCTTG
 GAGGCTCTGGAGACAATTATCGGGGCAAGGGTCGAGCTGGGGCAGTGGAGGAGGTGACGCTGTT
 GGTGGAGTCAATACTGTGAATCTGAGACGTCTCCTGGGATGTTTAACTTTGACACTTTCTGGAA
 GAATTTTAAATCCAAGCTGGGTTTCATCAACTGGGATGCCATAAACAAGGACCAGAGAAGCTCTC
 GCATCCCGTGACCTCCAGACAAGGAGCCACCAGATTGGATGGGAGCCCCACACTCCCTCCTTAA
 AACACCACCCTCTCATCACTAATCTCAGCCCTTGCCCTTGAAATAAACCTTAGCTGCCCCACAAA
 AA
 AA

[illegible]

MKFQGGLACLLLLALCLGSGEAGPLQSGEESTGTNIGEALGHGLGDALSEGVGKAIGKEAGGAAGSKVS
 EALGQGTREAVGTGVRQVPGFGAADALGNRVGEAAHALGNTGHEIGRQAEDEVIRHGADAVRGSWQGVF
 GHSGAWETSGGHGIFGSGQGLGGQGGNPGGLTGPVWHGYPGNSAGSFGMNPQGAPWQGGGNGGPPNF
 GTNTQGAVAQPGYGSVRASNQNEGCTNPPPSGGSGGSSNSGGSGSGSGSSGSGSNGDNNGSSSSGGS
 SSGSSSGSSSGSSGGSSGGSSGNSGGSRGDSGSESSWGSSTGSSSGNHGSGGGNGHKPGCEKPGNE
 ARGSGESGIQCFRGQGVSSNMREISKEGNRLLGSGSDNYRGQGSWSGGGDAVGGVNTVNSESPGM
 FNFDTFWKNFKSKLGFINWDAINKDORSSRIP

Signal peptide:

amino acids 1-21

N-glycosylation site.

amino acids 265-269

Glycosaminoglycan attachment site.

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

Casein kinase II phosphorylation site.

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

N-myristoylation site.

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70, 74-80,
90-96, 96-102, 130-136, 140-146, 149-155, 152-158, 155-161,
159-165, 163-169, 178-184, 190-196, 194-200, 199-205, 218-224,
236-242, 238-244, 239-245, 240-246, 245-251, 246-252, 249-252,
253-259, 256-262, 266-272, 270-276, 271-277, 275-281, 279-285,
283-289, 284-290, 287-293, 288-294, 291-297, 292-298, 295-301,
298-304, 305-311, 311-317, 315-321, 319-325, 322-328, 323-329,
325-331, 343-349, 354-360, 356-362, 374-380, 381-387, 383-389,
387-393, 389-395, 395-401

Cell attachment sequence.

amino acids 301-304

FIGURE 53

GGAGAAGAGGTTGTGTGGGACAAGCTGCTCCCCGACAGAAGGATGTCGCTGCTGAGCCTGCCCTGG
CTGGGCCTCAGACCGGTGGCAATGTCCCCATGGCTACTCCTGCTGCTGGTTGTGGGCTCCTGGCT
ACTCGCCCGCATCCTGGCTTGGACCTATGCCTTCTATAACAACAGCCGCGGCTCCAGTGTTC
CACAGCCCCAAAACGGAACGGTTTTGGGGTCACCTGGGCCTGATCACTCCTACAGAGGAGGGC
TTGAAGGACTCGACCCAGATGTGGGCCACCTATTCCCAGGGCTTTACGGTATGGCTGGGTCCCAT
CATCCCCCTTCATCGTTTTATGCCACCCTGACACCATCCGGTCTATCACCAATGCCTCAGCTGCCA
TTGCACCCAAGGATAATCTCTTCATCAGGTTCCCTGAAGCCCTGGCTGGGAGAAGGGATACTGCTG
AGTGGCGGTGACAAGTGGAGCCGCCACCGTCGGATGCTGACGCCCGCCTTCCATTTCAACATCCT
GAAGTCCTATATAACGATCTTCAACAAGAGTGCAAACATCATGCTTGACAAGTGGCAGCACCTGG
CCTCAGAGGGCAGCAGTCGTCTGGACATGTTTGAGCACATCAGCCTCATGACCTTGGACAGTCTA
CAGAAATGCATCTTCAGCTTTGACAGCCATTGTGAGGAGAGGGCCAGTGAATATATTGCCACCAT
CTTGAGCTCAGTGCCCTTGTAGAGAAAAGAAGCCAGCATATCCTCCAGCACATGGACTTTCTGT
ATTACCTCTCCCATGACGGGCGGCGCTTCCACAGGGCCTGCCGCTGGTGCATGACTTCACAGAC
GCTGTTCATCCGGGAGCGGCGTCGCACCTCCCCACTCAGGGTATTGATGATTTTTTCAAAGACAA
AGCCAAGTCCAAGACTTTGGATTTTATTGATGTGCTTCTGCTGAGCAAGGATGAAGATGGGAAGG
CATTGTCAGATGAGGATATAAGAGCAGAGGCTGACACCTTCATGTTTGAGGCCATGACACCAG
GCCAGTGGCCTCTCCTGGGTCTGTACAACCTTGCGAGGCACCCAGAATACCAGGAGCGCTGCCG
ACAGGAGGTGCAAGAGCTTCTGAAGGACCGCGATCCTAAAGAGATTGAATGGGACGACCTGGCCC
AGCTGCCCTTCTTGACCATGTGCGTGAAGGAGAGCCTGAGGTTACATCCCCAGCTCCCTTCATC
TCCCGATGCTGCACCCAGGACATTGTTCTCCAGATGGCCGAGTCATCCCCAAAGGCATTACCTG
CCTCATCGATATTATAGGGGTCCATCACAACCCAACTGTGTGGCCGGATCCTGAGGTCTACGACC
CCTTCCGCTTTGACCCAGAGAACAGCAAGGGGAGGTCACCTCTGGCTTTTATTCCCTTCTCCGCA
GGGCCCAGGAACTGCATCGGGCAGGCGTTCCGCATGGCGGAGATGAAAGTGGTCTGGCGTTGAT
GCTGCTGCACTTCCGGTTCCTGCCAGACCACACTGAGCCCCGCAGGAAGCTGGAATTGATCATGC
GCGCCGAGGGCGGGCTTTGGCTGCGGGTGGAGCCCTGAATGTAGGCTTGAGTGAAGTCTTCTGAC
CCATCCACCTGTTTTTTTGCAGATTGTCATGAATAAAACGGTGTGTCAA

FIGURE 54

MSLLSLPWLGLRPVAMSPWLLLLLVVGSWLLARILAWTYAFYNNCRRLQCFPPPKRNWFWGHLG
 LITPTEGLKDSTQMSATYSQGFTVWLGPIIPFIVLCHPDTIRSITNASAAIAPKDNLFIRFLKP
 WLGEILLSSGDKWSRHRRLTPAFHFNILKSYITIFNKSANIMLDKWQHLASEGSSRLDMFEHI
 SLMTLDSLQKCIFSFDSHCQERPSEYIATILELSALVEKRSQHILQHMDFLYYLSHDGRRFHRAC
 RLVHDFDVAVIRERRRTLPTQGIDDFFKDKAKSKTLDLFDVLLLSKDEDGKALSDEDIRAEADTF
 MFGGHDTTASGLSWVLYNLAHPEYQERCQEVQELLKDRDPKEIEWDDLAQLPFLTMCVKESLR
 LHPPAPFISRCCTQDIVLPDGRVIPKGITCLIDIIGVHHNPTVWPDPEVYDFFRDPENSKGRSP
 LAFIPFSAGPRNCIGQAFAMAEMKVVLALMLLHFRFLPDHTEPRRKLEIMRAEGGLWLRVEPLN
 VGLQ

Important features:

Transmembrane domains:

amino acids 13-32 (type II), 77-102

Cytochrome P450 cysteine heme-iron ligand signature.

amino acids 461-471

N-glycosylation sites.

amino acids 112-116, 168-172

FIGURE 55

[illegible]

FIGURE 56

MGPVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWWHNKGLALIFCILQSLALTWYLSFIPFAR
DAVKKCFVCLA

Important features:

Signal peptide:

amino acids 1-33

Type II fibronectin collagen-binding domain protein.

amino acids 30-72

FIGURE 57

CGGCTCGAGCTCGAGCCGAATCGGCTCGAGGGGAGTGGAGCAGCCAGCAGGCGGCCAACATGCTCTGTCTGTGCCTG
TACGTGCCGGTATCGGGGAAGCCAGACCGAGTTCCAGTACTTTGAGTCGAAGGGGCTCCCTGCCGAGCTGAAGTCC
ATTTTCAAGCTCAGTGTCTTATCCCTCCAGGAATTTCCACCTACCGCAGTGAAGCAGAAAAATGTACAAGCT
GGAGATAAGGACCTTGATGGGAGCTAGACTTTGAAGAATTTGTCCATTATCTCCAAGATCATGAGAAGAAGCTGAGG
CTGGTGTTTAAGATTTTGGACAAAAAGAAATGATGGACGCATTGACGCGCAGGAGATCATGCAGTCCCTGCCGGACTTG
GGAGTCAAGATATCTGAACAGCAGGCAGAAAAAATTTCTCAAGAGCATGGATAAAAAACGGCAGCATGACCATCGACTGG
AACGAGTGGAGAGACTACCACCTCTCCACCCCGTGGAAAAACATCCCGAGATCATCTCTACTGGAAGCATTCACG
ATCTTTGATGTGGGTGAGAACTAACGGTCCCGGATGAGTTACAGTGGAGGAGAGGCAGACGGGGATGTGGTGGAGA
CACCTGGTGGCAGGAGGTGGGGCAGGGCCGTATCCAGAACCTGCACGGCCCCCTGGACAGGCTCAAGGTGCTCATG
CAGGTCCATGCCTCCCGCAGCAACACATGGGCATCGTTGGTGGCTTCACTCAGATGATTGAGAAGGAGGGGCCAGG
TCACTTGGCGGGGCAATGGCATCAACGTCTCAAATTTGCCCCGAATCAGCCATCAAATTCATGGCTATGAGCAG
ATCAAGCGCCTTGTGGTAGTGACAGGAGACTCTGAGGATTCACGAGAGGCTTGTGGCAGGGTCCCTGGCAGGGGCC
ATCGCCAGAGCAGCATCTACCCAATGGAGGTCTGAAGACCCGGATGGCGCTGCCGAAGACAGGCCAGTACTCAGGA
ATGCTGGACTGGCCAGGAGGATCTGGCCAGAGAGGGGGTGGCCGCTTCTACAAAGGCTATGTCCCCAATGCTG
GGCATCATCCCTATGCCGGCATCGACCTTGCAGTCTACGAGAGGCTCAAGAAATGCCTGGCTGCAGCACTATGCAGTG
AACAGCGCGGACCCCGGCTGTTGTCTGCTGGCTGTGGCACCATGTCAGTACCTGTGGCCAGCTGGCCAGTAC
CCCCGGCCCTAGTCAGGACCCGGATGCAGGCGCAAGCCTTATTGAGGGCGCTCCGGAGTGACCATGAGCAGCCTC
TTCAAACATATCTTGGGACCGAGGGGGCTTGGGGTGTACAGGGGGCTGGCCCCCACTTCAAGAGGTATCCCA
GCTGTGAGCATCAGTACGTGGTCTACGAGAACTGAAGATCACCTGGGCGTGCACTCGCGGTGAACGGGGGAGGGC
CGCCCGGAGTGGACTCGCTGATCTGGGCGCAGCCTGGGGTGTGCAGCCATCTCATTCTGTGAATGTGCCAACT
AAGCTGTCTCGAGCCAAGCTGTGAAACCTAGACGACCCGAGGGAGGGTGGGAGAGCTGGCAGGCCAGGGCTT
GTCTGTGACCCAGCAGACCTCCTGTGGTTCAGCGAAGACCAAGGCATTCCTTAGGGTCCAGGGTCAGCAGG
CTCCGGGCTCAGATGTGTAAGGACAGGACATTTCTGCACTGCTGCCAATAGTGAGCTTGGAGCCTGGAGGCCGGCT
TAGTCTTCCATTACCCCTTGCAGCCAGCTGTGGCCACGGCCCTGCCCTGTGGTCTGCCGTGCATCTCCTGTGC
CTCTTGTCTGCTGCTGTCTGCTGAGGTAAGGTGGGAGGAGGGCTACAGCCACATCCCACCCCTCGTCCAATCCC
ATAATCCATGATGAAAGGTGAGGTACGCTGGCCTCCAGGCTGACTTCCCAACCTACAGATTGACGCCAATTTGGC
TGTGAAGGAAGAGGAAGGATCTGGCCTTGTGGTCACTGGCATCTGAGCCCTGCTGATGGCTGGGGCTCTCGGGCATG
CTTGGGAGTGCAGGGGGCTCGGGCTGCTGGCTGGCTGCACAGAAGGCAAGTGTGGGGCTCATGGTGTCTGAGCT
GGCCTGGACCTGTGAGGATGGGCCCCACCTCAGAACCAACTCACTGTCCCACTGTGGCATGAGGGCAGTGGAGCA
CCATGTTTGAAGGCGAAGGGCAGAGCGTTTGTGTGTTCTGGGGAGGGAAGGAAAAGTGTGGAGGCCCTTAATTATGG
ACTGTTGGGAAAAGGGTTTGTCCAGAAGGACAAGCCGACAAATGAGCGACTTCTGTGCTTCCAGAGGAAGACGAGG
GAGCAGGAGCTTGGCTGACTGCTCAGAGTCTGTTCTGACGCCCTGGGGGTCTCTGTCCAACCCAGCAGGGGGCAGC
GGGACAGCCCCACATTCCACTTGTGTCACTGCTTGAACCTATTATTTTGTATTATTGAACAGAGTTATGTCTCT
AACTATTTTATAGATTTGTTAATTAATAGCTTGTCAATTTCAAGTTTCAATTTTATTCATATTATGTTTATGTT
GATTGTACCTTCCCAAGCCCGCCAGTGGGATGGGAGGAGGAGGAGAAGGGGGCTTGGGCGCTGCAGTCACATCT
GTCCAGAGAAATTCCTTTTGGGACTGGAGGCAGAAAAGCGGCCAGAAGGCAGCAGCCCTGGCTCCTTTCTTTGGCAG
GTTGGGGAGGGCTTGGCCCCAGCCTTAGGATTTCAAGGTTTGAATGGGGCTGGAGAGAGAGGAGGAACCTCAAT
AACCTTGAAGGTGGAATCCAGTTATTTCTGCGCTGCGAGGGTTCTTTATTTCACTCTTTCTGAATGTCAAGGCAG
TGAGGTGCCTCTCACTGTGAATTTGTGGTGGGCGGGGGCTGGAGGAGAGGGTGGGGGGCTGGCTCCGCTCCCTCCAGC
CTTCTGCTGCCCTTGTCTAACAAATGCCGGCAACTGGCGACCTCACGGTGTCACTTCCATTCCACCAGAAATGACCTGA
TGAGGAAATCTCAATAGGATGCAAGATCAATGCAAAAATTTGTTATATATGAACATATAACTGGAGTCGTCAAAAAG
CAAAATTAAGAAAAGAAATGGACGTTAGAAGTTGTCAATTTAAAGCAGCCTTCAATAAAGTTGTTTCAAGCTGAAAAA
AA

FIGURE 58

MLCLCLYVPVIGEAQTEFQYFESKGLPAELKSIIFKLSVFIPSQEFSTYRQWKQKIVQAGDKDLDG
 QLDFFEFEVHYLQDHEKKLRLVFKILDKKNDGRIDAQEQSLRDLGVKISEQQAEEKILKSMCKNG
 TMTIDWNEWRDYHLLHPVENIPEIILYWKHSTIFDVGENLTPDEFTVEERQTGMWWRHLVAGGG
 AGAVSRTCTAPLDRKVLQMVFHASRSNNMGIVGGFTQMIREGGARSLWRGNGINVLKIAPESAIAK
 FMAYEQIKRLVGSDQETLRIHERLVAGSLAGAIQSSIIYPMEVLKTRMALRKTGQYSGMLDCARR
 ILAREGVAAFYKGYVPNMLGIIPYAGIDLAVYETLKNWLQHYAVNSADPGVFVLLACGTMSSTC
 GQLASYPLALVRTRMQAASIEGAPEVTMSSLFKHILRTEGAFGLYRGLAPNFMKVIPAVSISYV
 VYENLKITLGVQSR

Important features:**Signal peptide:**

amino acids 1-16

Putative transmembrane domains:

amino acids 284-304, 339-360, 376-394

Mitochondrial energy transfer proteins signature.

amino acids 206-215, 300-309

N-glycosylation sites.

amino acids 129-133, 169-173

Elongation Factor-hand calcium-binding protein.

amino acids 54-73, 85-104, 121-140

FIGURE 59

GGAAGGCAGCGGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGGAACCTTCCCCAGCCATGGC
TTCCCTGGGGCAGATCCTCTTCTGGAGCATAATTAGCATCATCATTATTCTGGCTGGAGCAATTG
CACTCATCATTGGCTTTGGTATTTAGGGAGACACTCCATCACAGTCACTACTGTGCGCTCAGCT
GGGAACATTGGGGAGGATGGAATCCTGAGCTGCACTTTTGAACCTGACATCAAACCTTTCTGATAT
CGTGATACAATGGCTGAAGGAAGGTGTTTTAGGCTTGGTCCATGAGTTCAAAGAAGGCAAAGATG
AGCTGTGCGGAGCAGGATGAAATGTTGAGAGCCGGACAGCAGTGTTTGCTGATCAAGTGATAGTT
GGCAATGCCTCTTTGCGGCTGAAAAACGTGCAACTCACAGATGCTGGCACCTACAAATGTTATAT
CATCACTTCTAAAGCAAGGGGAATGCTAACCTTGAGTATAAACTGGAGCCTTCAGCATGCCGG
AAGTGAATGTGGACTATAATGCCAGCTCAGAGACCTTGCGGTGTGAGGCTCCCCGATGGTTCCCC
CAGCCCACAGTGGTCTGGGCATCCCAAGTTGACCAGGGAGCCAACCTTCTCGGAAGTCTCCAATAC
CAGCTTTGAGCTGAACTCTGAGAATGTGACCATGAAGGTTGTGTCTGTGCTCTACAATGTTACGA
TCAACAACACATACTCCTGTATGATTGAAAATGACATTGCCAAAGCAACAGGGGATATCAAAGTG
ACAGAAATCGGAGATCAAAAGGCGGAGTCACCTACAGCTGCTAAACTCAAAGGCTTCTCTGTGTGT
CTCTTCTTTCTTTGCCATCAGCTGGGCACCTTCTGCCTCTCAGCCCTTACCTGATGCTAAAAATAAT
GTGCCTTGCCACAAAAAGCATGCAAAGTCATTGTTACAACAGGGATCTACAGAATATTTCAC
CACCAGATATGACCTAGTTTTATATTTCTGGGAGGAAATGAATTCATATCTAGAAGTCTGGAGTG
AGCAAACAAGAGCAAGAAACAAAAAGAAGCCAAAAGCAGAAGGCTCCAATATGAACAAGATAAAT
CTATCTTCAAAGACATATTAGAAGTTGGGAAAATAATTCATGTGAAGTAGACAAGTGTGTTAAGA
GTGATAAGTAAATGCACGTGGAGACAAGTGCATCCCCAGATCTCAGGGACCTCCCCCTGCCTGT
CACCTGGGGAGTGAGAGGACAGGATAGTGCATGTTCTTTGTCTCTGAATTTTTAGTTATATGTGC
TGTAATGTTGCTCTGAGGAAGCCCTGGAAAGTCTATCCCAACATATCCACATCTTATATTCCAC
AAATTAAGCTGTAGTATGTACCCTAAGACGCTGCTAATTGACTGCCACTTCGCAACTCAGGGGCG
GCTGCATTTTAGTAATGGGTCAAATGATTCACTTTTTATGATGCTTCCAAAGGTGCCTTGCGCTTC
TCTTCCCAACTGACAAATGCCAAAGTTGAGAAAAATGATCATAATTTTAGCATAAACAGAGCAGT
CGGGGACACCGATTTTATAAATAAACTGAGCACCTTCTTTTTAAACAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 6o

MASLGQILFWSIIISIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDIKLS
DIVIQWLKEGVLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASLRLKNVQLTDAGTYKC
YIITSKGKGNANLEYKTGAFSMPEVNVVDYNASSETLRCEAPRWFPQPTVVWASQVDQGANFSEVS
NTSFELNSENVTMKVSVLYNVTINNTYSCMIENDIAKATGDIKVTSEIKRRSHLQLLNSKASL
CVSSFFAISWALLPLSPYMLK

Important features:**Signal peptide:**

amino acids 1-28

Transmembrane domain:

amino acids 258-281

N-glycosylation sites.

amino acids 112-116, 160-164, 190-194, 196-200, 205-209, 216-220,
220-224

N-myristoylation sites.

amino acids 52-58, 126-132, 188-194

FIGURE 61

TGACGTCAGAATCACCATGGCCAGCTATCCTTACCGGCAGGGCTGCCAGGAGCTGCAGGACAAG
 CACCAGGAGCCCCTCCGGGTAGCTACTACCCTGGACCCCCCAATAGTGGAGGGCAGTATGGTAGT
 GGGCTACCCCCTGGTGGTGGTTATGGGGTCTGCCCCCTGGAGGGCCTTATGGACCACCAGCTGG
 TGGAGGGCCCTATGGACACCCCAATCCTGGGATGTTCCCCCTCTGGAACCTCAGGAGGACCATATG
 GCGGTGCAGCTCCCGGGGGCCCCCTATGGTCAGCCACCTCCAAGTTCCTACGGTGCCAGCAGCCT
 GGGCTTTATGGACAGGGTGGCGCCCCCTCCCAATGTGGATCCTGAGGCCTACTCCTGGTTCCAGTC
 GGTGGACTCAGATCACAGTGGCTATATCTCCATGAAGGAGCTAAAGCAGGCCCTGGTCAACTGCA
 ATTGGTCTTCATTCAATGATGAGACCTGCCTCATGATGATAAACATGTTTGACAAGACCAAGTCA
 GGCCGCATCGATGTCTACGGCTTCTCAGCCCTGTGAAATTCATCCAGCAGTGAAGAACCTCTT
 CCAGCAGTATGACCGGGACCGCTCGGGCTCCATTAGCTACACAGAGCTGCAGCAAGCTCTGTCCC
 AAATGGGCTACAACCTGAGCCCCAGTTCACCCAGCTTCTGGTCTCCCGCTACTGCCACGCTCT
 GCCAATCCTGCCATGCAGCTTGACCGCTTCATCCAGGTGTGCACCCAGCTGCAGGTGCTGACAGA
 GGCTTCCGGGAGAAGGACACAGCTGTACAAGGCAACATCCGGCTCAGTTTCGAGGACTTCGTCA
 CCATGACAGCTTCTCGGATGCTATGACCCAACCATCTGTGGAGAGTGGAGTGCACCAGGGACCTT
 TCCTGGCTTCTTAGAGTGAGAGAAGTATGTGGACATCTCTTCTTTCTGTCCCTCTAGAAGAAC
 ATTCTCCCTTGCTTGATGCAACACTGTTCCAAAAGAGGGTGGAGAGTCTGCATCATAGCCACCA
 AATAGTGAGGACCGGGCTGAGGCCACACAGATAGGGGCTGATGGAGGAGAGGATAGAAGTTGA
 ATGTCCTGATGGCCATGAGCAGTTGAGTGGCACAGCCTGGCACCAGGAGCAGGTCCTTGTAATGG
 AGTTAGTGTCAGTCAGCTGAGCTCCACCCTGATGCCAGTGGTGAGTGTTCATCGGCCTGTTACC
 GTTAGTACCTGTGTTCCCTCACCAGGCCATCCTGTCAAACGAGCCCATTTTCTCCAAAGTGGAAT
 CTGACCAAGCATGAGAGAGATCTGTCTATGGGACCAGTGGCTTGGATTCTGCCACACCCATAAAT
 CCTTGTTGTTAACTTCTAGCTGCCTGGGGCTGGCCCTGCTCAGACAAATCTGCTCCCTGGGCAT
 CTTTGGCCAGGCTTCTGCCCCCTGCAGCTGGGACCCCTCACTTGCTGCCATGCTCTGCTCGGCT
 TCAGTCTCCAGGAGACAGTGGTCACCTCTCCCTGCCAATACTTTTTTTAATTTGCATTTTTTTTC
 ATTTGGGGCCAAAAGTCCAGTGAAATTGTAAGCTTCAATAAAAGGATGAAACTCTGA

FIGURE 62

MASYPYRQGPCGAAGQAPGAPPGSYYPGPPNSGGQYGSGLPPGGGYGGPAPGGPYGPPAGGGPYG
HPNPGMFPSGTPGGPYGGAAPGGPYGQPPSSYGAQQPGLYGQGGAPPNVDPEAYSWFQSVDS DH
SGYISMKELKQALVNCNWSSFNDETCLMMINMFDKTKSGRIDVYGFSALWKFIQQWKNLFQQYDR
DRSGSISYTELQQALSQMGYNLSPQFTQLLVSRYPERSANPAMQLDRFIQVCTQLQVLTEAFREK
DTAVQGNIRLSFEDFVTMTASRML

Important features of the protein:

Signal peptide:

amino acids 1-19

N-glycosylation site.

amino acids 147-150

Casein kinase II phosphorylation sites.

amino acids 135-138, 150-153, 202-205, 271-274

N-myristoylation sites.

amino acids 9-14, 15-20, 19-24, 33-38, 34-39, 39-44, 43-48, 61-
66, 70-75, 78-83, 83-88, 87-92, 110-115

FIGURE 63

CAGGATGCAGGGCCGCGTGGCAGGGAGCTGCGCTCCTCTGGGCGCTGCTCCTGGTCTGTCTTCATC
TCCCAGGCCTCTTTGCCCCGAGCATCGGTGTTGTGGAGGAGAAAGTTTCCCAAACTTCGGGACC
AACTTGCCCTCAGCTCGGACAACCTTCCTCCACTGGCCCCCTAACTCTGAACATCCGCAGCCCGC
TCTGGACCCTAGGTCTAATGACTTGGCAAGGGTTCTCTGAAGCTCAGCGTGCCTCCATCAGATG
GCTTCCCACCTGCAGGAGGTTCTGCAGTGCAGAGGTGGCCTCCATCGTGGGGGCTGCCTGCCATG
GATTCTGGCCCCCTGAGGATCCTTGGCAGATGATGGCTGCTGCGGCTGAGGACCGCCTGGGGGA
AGCGCTGCCTGAAGAACTCTTTACCTCTCCAGTGCTGCGGCCCTCGCTCCGGGCAGTGGCCCTT
TGCCTGGGGAGTCTTCTCCCGATGCCACAGGCCTCTCACCTGAGGCTTCACTCCTCCACCAGGAC
TCGGAGTCCAGACGACTGCCCCGTTCTAATTCAGTGGGAGCCGGGGAAAAATCCTTTCCCAACG
CCCTCCCTGGTCTCTCATCCACAGGGTTCTGCCTGATCACCCCTGGGGTACCCTGAATCCCAGTG
TGTCCTGGGGAGGTGGAGGCCCTGGGACTGGTTGGGGAACGAGGCCCATGCCACACCCTGAGGGA
ATCTGGGGTATCAATAATCAACCCCAGGTACCAGCTGGGGAAATATTAATCGGTATCCAGGAGG
CAGCTGGGGAAATATTAATCGGTATCCAGGAGGCAGCTGGGGGAATATTAATCGGTATCCAGGAG
GCAGCTGGGGGAATATTCATCTATAACCCAGGTATCAATAACCCATTTCTCCTGGAGTTCTCCGC
CCTCCTGGCTCTTCTTGAACATCCCAGCTGGCTTCCCTAATCTCCAAGCCCTAGGTTGCAGTG
GGGCTAGAGCACGATAGAGGGAAACCAACATTGGGAGTTAGAGTCTGCTCCCGCCCCCTTGCTG
TGTGGGCTCAATCCAGGCCCTGTTAACATGTTTCCAGCACTATCCCCACTTTTCAGTGCCTCCCC
TGCTCATCTCCAATAAAATAAAAGCACTTATGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAA

FIGURE 64

MQGRVAGSCAPLGLLLVCLHPLGLFARSIGVVEEKVSQNFGTNLPQLGQPSSTGSPNSEHPQPAL
DPRSNDLARVPLKLSVPPSDGFPPAGGSQVQRWPPSWGLPAMDSWPPEDPWQMAAAAEDRLGEA
LPEELSYLSSAAALAPGSGPLPGESSPDATGLSPEASLLHQDSESRRLPRSNSLGAGGKILSQRP
PWSLIHRVLPDHPWGTLNPSVSWGGGGPGTGWGTRMPHPHEGIWGINNQPPGTSGWGNINRYPGGS
WGNINRYPGGSWGNINRYPGGSWGNIHLYPGINNPFPFPGVLRPPGSSWNI PAGFPNPPSPRLQWG

Important features of the protein:

Signal peptide:

amino acids 1-26

Casein kinase II phosphorylation sites.

amino acids 56-59, 155-158

N-myristoylation sites.

amino acids 48-53, 220-225, 221-226, 224-229, 247-252, 258-263,
259-264, 269-274, 270-275, 280-285, 281-286, 305-310

FIGURE 65

AAGGAGAGGCCACCGGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACTTATGGGGTC
TGGGCTGCCCCCTTGTCTCCTCTTGACCCTCCTTGGCAGCTCACATGGAACAGGGCCGGGTATGA
CTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGCTTCCTGGAA
TTGCTTGAAAAGCTCTGCCTCCTCCTCCATCTCCCTTCAGGGACCAGCGTCACCCTCCACCATGC
AAGATCTCAACACCATGTTGTCTGCAACACATTGACAGCCATTGAAGCCTGTGTCTTCTTGGCCC
GGGCTTTTGGGCCGGGGATGCAGGAGGCAGGCCCCGACCCTGTCTTTTACAGCAGGCCCCCACCTC
CTGAGTGGCAATAAATAAAATTCGGTATGCTG

FIGURE 66

MGSGPLPLVLLLTLLGSSHGTGPGMTLQKLKESFLTNSSESSFLELLEKLCLLLHLPSGTSVTL
HHARSQHHVVCNT

Important features:

Signal peptide:

amino acids 1-19

N-glycosylation site.

amino acids 37-41

N-myristoylation sites.

amino acids 15-21, 19-25, 60-66

FIGURE 67

ACGGACCGAGGGTTCGAGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCCGGGC
 CAGGTGCCCCGTGCGCAGGTGCCCCCTGGCCGGAGATGCGGTAGGAGGGGCGAGCGCGAGAAGCCCC
 TTCCTCGGCGCTGCCAACCCGCCACCCAGCCCATGGCGAACCCCGGGCTGGGGCTGCTTCTGGCG
 CTGGGCCTGCCGTTCTGCTGGCCCGCTGGGGCCGAGCCTGGGGGCAAATACAGACCACTTCTGC
 AAATGAGAATAGCACTGTTTTGCCTTCATCCACCAGCTCCAGCTCCGATGGCAACCTGCGTCCGG
 AAGCCATCACTGCTATCATCGTGGTCTTCTCCCTCTTGGCTGCCTTGCTCCTGGCTGTGGGGCTG
 GCACTGTTGGTGCGGAAGCTTCGGGAGAAGCGGCAGACGGAGGGCACCTACCGGCCCACTAGCGA
 GGAGCAGTTCTCCCATGCAGCCGAGGCCCGGGCCCTCAGGACTCCAAGGAGACGGTGCAGGGCT
 GCCTGCCCATCTAGGTCCCCCTCTCCTGCATCTGTCTCCCTTCATTGCTGTGTGACCTTGGGGAAA
 GGCAGTGCCCTCTCTGGGCAGTCAGATCCACCCAGTGCTTAATAGCAGGGAAGAAGGTACTTCAA
 AGACTCTGCCCCTGAGGTCAAGAGAGGATGGGGCTATTCACTTTTATATATTTATATAAAATTAG
 TAGTGAGATGTAAAAAAAAAAAAAAAAAAAA

FIGURE 68

MANPGLGLLLALGLPFLLARWGRAWGQIQTTSANENSTVLPSSSTSSSSDGNLRPEAITAIIVVFS
LLAALLLAVGLALLVRKLRKQTEGTYRPSSEEQFSHAAEARAPQDSKETVQGCLPI

Important features:

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 56-80

N-glycosylation site.

amino acids 36-40

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 86-90

Tyrosine kinase phosphorylation site.

amino acids 86-94

N-myristoylation sites.

amino acids 7-13, 26-32

FIGURE 69

GCCAGGAATAACTAGAGAGGAACAATGGGGTTATTTCAGAGGTTTTGTTTTCTCTTAGTTCTGTGCCTGCTGCACCAG
TCAAATACTTCCCTTCATTAAGCTGAATAATAATGGCTTTGAAGATATTGTCATTGTTATAGATCCTAGTGTGCCAGAA
GATGAAAAATAATTAACAAATAGAGGATATGGTGACTACAGCTTCTACGTACCTGTTTGAAGCCACAGAAAAAGA
TTTTTTTTCAAAAATGTATCTATATTAATTCCTGAGAATTGGAAGGAAAAATCCTCAGTACAAAAGGCCAAAAATGAA
AACCATAAACATGCTGATGTTATAGTTGCACCACCTACACTCCAGGTAGAGATGAACCATACACCAAGCAGTTTACA
GAATGTGGAGAGAAAGGCGAATACATTCACTTCACCCTGACCTTCTACTTGGAAAAAACAAAATGAATATGGACCA
CCAGGCAAACTGTTTGTCCATGAGTGGGCTCACCTCCGGTGGGGAGTGTGATGAGTACAATGAAGATCAGCCTTTC
TACCGTGCTAAGTCAAAAAAATCGAAGCAACAAGGTGTTCCGCAGGTATCTCTGGTAGAAAATAGAGTTTATAAGTGT
CAAGGAGGCAGCTGCTTAGTAGAGCATGCGAATTGATTCTACAACAAAACGTGTATGGAAAAAGATTGCAATTCTTT
CCTGATAAAGTACAAACAGAAAAAGCATCCATAATGTTATGCAAAGTATTGATTCTGTTGTTGAATTTGTAACGAA
AAAACCCATAATCAAGAAGCTCCAAGCCTACAAAACATAAAGTGCAATTTTAGAAGTACATGGGAGGTGATTAGCAAT
TCTGAGGATTTTAAAAACACCATAACCCATGGTGACACCACCTCCTCCACCTGTCTTCTCATTGCTGAAGATCAGTCAA
AGAATTGTGTGCTTAGTTCTTGATAAGTCTGGAAGCATGGGGGTAAGGACCGCCTAAATCGAATGAATCAAGCAGCA
AAACATTTTCTGCTGCAGACTGTTGAAAAATGGATCCTGGGTGGGGATGGTTCACTTTGATAGTACTGCCACTATTGTA
AATAAGCTAATCCAAATAAAAGCAGTGATGAAAGAAACACACTCATGGCAGGATTACCTACATATCCTCTGGGAGGA
ACTTCCATCTGCTCTGGAATTAAATATGCATTTCAAGTGATGGAGAGCTACATTCCCAACTCGATGGATCCGAAGTA
CTGCTGCTGACTGATGGGGAGGATAACACTGCAAGTTCTTGATTGATGAAGTGAACAAAGTGGGGCATTGTTTCAT
TTTATTGCTTTGGGAAGAGCTGCTGATGAAGCAGTAATAGAGATGAGCAAGATAACAGGAGGAAGTCATTTTATGTT
TCAGATGAAGCTCAGAACAATGGCCTCATTGATGCTTTTGGGGCTCTTACATCAGGAAATACTGATCTCTCCAGAAAG
TCCCTTCAGCTCGAAAGTAAGGGATTAACTGAATAGTAATGCCTGGATGAACGACACTGTCAATAATTGATAGTACA
GTGGGAAAGGACAGCTTCTTCTCATCACATGGAACAGCTGCTGCCAGTATTCTCTCTGGGATCCAGTGGAACA
ATAATGGAAAAATTCACAGTGGATGCAACTTCCAAATGGCCTATCTCAGTATTCCAGGAAGTCAAAAGTGGGCAT
TGGGCATACAATCTTCAAGCCAAAGCGAACCAGAAACATTAACTATTACAGTAACTTCTCGAGCAGCAAAATCTTCT
GTGCCTCCAATCACAGTGAATGCTAAATGAATAAGGACGTAAACAGTTTCCCAGCCCAATGATTGTTACGCAGAA
ATTCTACAAGGATATGTACCTGTTCTTGGAGCCAATGTGACTGCTTTCATTGAATCACAGAATGGACATACAGAAGTT
TTGGAACCTTTGGATAATGGTGCAGGCGCTGATTCTTTCAAGAAATGATGGAGTCTACTCCAGGTATTTACAGCATAT
ACAGAAAATGGCAGATATAGCTTAAAGTTCCGGCTCATGGAGGAGCAAACTGCCAGGCTAAAATACGGCTCCA
CTGAATAGAGCCGCTACATACCAGGCTGGGTAGTGAACGGGGAAATTGAAGCAAAACCCGCAAGACCTGAAATTGAT
GAGGATACTCAGACCACCTTGGAGGATTTAGCCGAAACAGCATCCGGAGGTGCAATTTGTGGTATCACAAAGTCCCAAGC
CTTCCCTTGCCTGACCAATACCCACCAAGTCAAATCACAGACCTTGATGCCACAGTTTATGAGGATAAGATTATCTT
ACATGGACAGCACCAGGAGATAATTTGATGTTGAAAAAGTTCAACGTTATATCATAAGAATAAGTGAAGTATTCTT
GATCTAAGAGACAGTTTTGATGATGCTTCAAGTAAATACTACTGATCTGTCAACAAAGGAGGCCAACTCCAAAGGAA
AGCTTTGCATTAAACAGAAAAATATCTCAGAAGAAAAATGCAACCCACATATTATTGCCATTAAAGATATAGATAAA
AGCAATTTGACATCAAAAGTATCCAACATTGCACAAGTAACTTTGTATTATCCCTCAAGCAAAATCCTGATGACATTGAT
CCTACACCTACTCCTACTCCTACTCCTGATAAAAGTCATAATCTGGAGTTAATATTTCTACGCTGGTATTG
TCTGTGATTGGGTCTGTTGTAATTGTTAACTTTATTTTAAGTACCACCTTTGAACCTTAACGAAGAAAAAATCTTC
AAGTAGACCTAGAAGAGAGTTTTAAAAAACAAAACATGTAAGTAAAGGATATTCTGAATCTTAAATTCATCCCAT
GTGTGATCATAACTCATAAAAATAATTTAAGATGTCGGAAGGATACTTTGATTAAATAAAAAACACTCATGGATA
TGTAAAAACTGTCAAGATTAATTTAATAGTTTCATTTATTGTTATTATTGTAAGAAATAGTGATGAACAAAG
ATCCTTTTTCTACTGATACCTGGTTGATATTATTGATGCAACAGTTTTCTGAAATGATATTTCAAATGTCATCAA
GAAATTAATCATCTATCTGAGTAGTCAAAATACAAGTAAAGGAGCAAAATAACCAACATTTGGAAAAA
AA

FIGURE 70

MGLFRGFVFLVLCLLHQSNTSFIKLNNGFEDIVIVIDPSVPEDEKIEQIEDMVTASTYLFE
 ATEKRFFFKNVSILIPENWKENPOYKRPKHENHKHADVIVAPPTLPGRDEPYTKQFTECGEKGEY
 IHFTPDLLLGGKQNEYGPPGKLFVHEWAHLRWGVFDEYNEDQPFYRAKSKKIEATRCISAGISGRN
 RVYKCQGGSCLSRACRIDSTTKLYGKDCQFFPDKVQTEKASIMFMQSIDSVVEFCNEKTHNQEAP
 SLQNIKCNFRSTWEVISNSEDFKNTIPMVTPPPPVFSLLKISQRIVCLVLDKSGSMGGKDRLNR
 MNQAAKHFLQLTVENGSWVGMVHFDSTATIVNKLIQIKSSDERNTLMAGLPTYPLGGTSICSGIK
 YAFQVIGELHSQLDGSEVLLLTGDNATASSCIDEVKQSGAIVHFIALGRAADEAVIEMSKITGG
 SHFYVSDEAQNNGLIDAFGALTSGNTDLSQKSLQLESKGLTLNSNAWMNDTVIIDSTVGKDTFFL
 ITWNSLPPSISLWDPSTIMENFTVDATSKMAYLSIPGTAKVGWTWAYNLQAKANPETLTITVTSR
 AANSSVPPITVNAKMNDVNSFSPMIVYAEILQGYVPVLGANVTAFIESQNGHTEVLELLDNGA
 GADSFKNMGVYSRYFTAYTENGRYSLKVRHGGANTARLKLRPPLNRAAYIPGWVVNGEIEANPP
 RPEIDEDTQTTLDFSRASGGAFVVSQVPSLPLPDQYPPSQITDLDTVHEDKIIILWTAPGDN
 FVDGKVQRYIIRISASILDLRDSFDDALQVNTDLSPEANSKESFAFKPENISEENATHIFIAI
 KSIDKSNLTSKVSNIAQVTLFIPQANPDDIDPTPTPTPTPTDKSHNSGVNISTLVLSVIGSVVI
 VNFILSTTI

Signal peptide:

amino acids 1-21

Putative transmembrane domains:

amino acids 284-300, 617-633

Leucine zipper pattern.

amino acids 469-491, 476-498

N-glycosylation site.
 amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592,
 628-632, 811-815, 832-836, 837-841, 852-856, 896-900

FIGURE 71

CTCCTTAGGTGGAAACCCTGGGAGTAGAGTACTGACAGCAAAGACCGGGAAAGACCATACGTCCCCGGGAGGGGTGA
CAACAGGTGTCATCTTTTGAATCTCGTGTGGCTGCCTTCTATTTCAAGGAAAGACGCCAAGGTAATTTTGACCCA
GAGGAGCAATGATGTAGCCACCTCCTAACCTTCCCTTCTTGAACCCCAAGTTATGCCAGGATTTACTAGAGAGTGTCA
ACTCAACCAGCAAGCGGCTCCTTCGGCTTAACCTTGTGGTTGGAGGAGAGAACCTTTGTGGGGCTGCGTTCTCTTAGCA
GTGCTCAGAAGTGACTTGCCTGAGGGTGGACCAGAAAGGAAAGGTTCCCTCTTGTCTTGGCTGCACATCAGGAA
GGCTGTGATGGGAATGAAGGTGAAAACCTTGGAGATTTCACTTCAGTCATTGCTTCTGCCTGCAAGATCATCCTTTAAA
AGTAGAGAAGCTGCTCTGTGTGGTGGTTAACTCCAAGAGGCGAAGCTCGTTCTAGAAGGAAATGGATGCAAGCAGCTC
CGGGGGCCCCAAACGCATGCTTCTGTGGTCTAGCCCAGGGAAGCCCTTCCGTGGGGGCCCCGGCTTTGAGGGATGCC
ACCGGTTCTGGACGCATGGCTGATTCTGATGATGTTTCCGCGGGGGCTGCTTGCCTGGATTTCGCGGGTGGTG
GTTTTGCTGGTGCTCCTCTGCTGTGCTATCTCTGCTGTACATGTTGGCTGCACCCAAAGGTGACGAGGAGCAG
CTGGCAGTCCCCAGGGCCAAACAGCCCAAGGGGAAGGAGGGGTACCAGGCCGCTCTTCAGGAGTGGGAGGAGCAGCAG
CGCAACTACGTGAGCAGCTGAAGCGGCAGATCGCACAGCTCAAGGAGGAGCTGCAGGAGAGGAGTGAGCAGCTCAGG
AATGGGCAGTACCAAGCCAGCGATGCTGCTGGCTTGGACAGGAGCCCGCCAGAGAAAACCCAGGCCGACCTC
CTGGCCTTCTGCACTCGCAGGTGGACAAGGAGGAGTGAATGCTGGCGTCAAGCTGGCCACAGAGTATGCAGCAGTG
CCTTTCGATAGCTTACTCTACAGAAAGGTGTACCAGCTGGAGACTGGCCTTACCCGCCACCCCGAGGAGAGCTGTG
AGGAAGGACAAGCGGGATGATTGGTGGAAAGCCATTGAATCAGCCTTGGAGACCCTGAACATCCTGACAGAACAGC
CCCAATCACCGTCTTACAGGCCCTCTGATTTCATAGAAGGGATCTACCAACAGAAAGGGACAAAGGGACATTGTAT
GAGCTCACCTTCAAAGGGGACCAAAACACGAATTCAAACGGCTCATCTTATTCGACCATTTCAGCCCCATCATGAAA
GTGAAAATGAAAAGCTCAACATGGCCAAACACGCTTATCAATGTTATCGTGCCTTAGCAAAAAGGGTGGACAGTTTC
CGGCAGTTCTGCGAGAATTTAGGGAGATGTGCATTGAGCAGGATGGGAGAGTCCATCTCACTGTTGTTTACTTTGGG
AAAGAAGAAATAAATGAAGTCAAAGGAATACTTGAAGAACCTTCAAAGCTGCCAATTTCAGGAATTTACCTTCATC
CAGCTGAATGGAGAATTTCTCGGGGAAAGGGACTTGATGTTGGAGCCCGCTTCTGGAAGGGAAGCAACCTCCTTCTC
TTTTCTGTGATGTGCACATCTACTTCACATCTGAATTCCTCAATACGTGTAGGCTGAATACACAGCCAGGGAAGAAG
GTATTTTATCCAGTTCTTTTCAGTCACTAATCCTGGCATAATATACGGCCACCATGATGCAGTCCCTCCCTTGGAA
CAGCAGCTGGTCATAAAGAAGGAACTGGATTTTGGAGAGACTTTGGATTGGGATGACGTGTAGTATCGGTGAGAC
TTATCAATATAGGTGGGTTTGTATCTGGACATCAAAGGCTGGGGCGGAGAGGATGTGCACCTTTATCGCAAGTATCTC
CACAGCAACCTCATAGTGTACGGACGCTGTGCGAGGACTCTCCACCTCTGGCATGAGAAGCGCTGCATGGACGAG
CTGACCCCGAGCAGTACAAGATGTGCATGCACTCCAAGGCCATGAACGAGGCATCCACGGCCAGCTGGGCATGCTG
GTGTTCAAGCAGCAGATAGAGGCTCACCTTCGCAACAGAAACAGAAAGACAAGTAGCAAAAAACATGAATCCCGAGA
GAAGGATTGTGGGAGACACTTTTCTTCTTCTTTTGAATTAAGTGGCTGCAACAGAGAAAAGACTTCCATAAA
GGACGACAAAAGAATTGGACTGATGGGTGAGAGATGAGAAGCCTCCGATTTCTCTCTGTTGGGCTTTTACAACAGA
AATCAAAATCTCCGCTTTGCCTGCAAAAGTAACCCAGTTGCACCCCTGTGAAGTGTCTGACAAGGCAGAAATGCTTGTG
AGATTATAAGCCTAATGGTGTGGAGTTTGTATGGTGTTTACAATACACTGAGACCTGTTGTTTTGTGTGCTCATTGA
AATATTCATGATTTAAGAGCAGTTTGTAAAAAATTCATTAGCATGAAGGCAAGCATATTTCTCCCTCATATGAATGA
GCCTATCAGCAGGGCTCTAGTTTCTAGGAATGCTAAAATATCAGAAGGCAGGAGAGGAGATAGGCTTATTATGATACT
AGTGATACATTAAGTAAATAAAATGGACCAGAAAAGAAAAGAAACCATAAATATCGTGTATATTTCCCCAAGAT
TAACCAAAAATAATCTGCTTATCTTTTGGTGTCTTTTAACTGTCTCCGTTTTTTCTTTTATTTAAAAATGCACT
TTTTTCTCCTTGTGAGTTATAGTCTGCTTATTTAATTACCACCTTTCGAAGCCTTACAAGAGAGCACAAGTTGGCCTAC
ATTTTTATATTTTTTAAGAAGTACTTTGAGATGCATTATGAGAATTTTCAGTTCAAAGCATCAAATGTATGCCATAT
CCAAGGACATGCCAAATGCTGATTCTGTGAGGCACTGAATGTGAGGCATTGAGACATAGGGAAGGAATGGTTGTACT
AATACAGACGTACAGATACTTTCTCTGAAGAGTATTTTGAAGAGGAGCAACTGAACACTGGAGGAAAAGAAAATGAC
ACTTTCTGCTTTACAGAAAAGGAACTCATTACAGACTGGTGATATCGTGATGTACCTAAAAGTCAGAAACCACATTTT
CTCCTCAGAAGTAGGACCGCTTTCTTACCTGTTTAAATAAACCAAGATATACCGTGTGAACCAAAACATCTCTTTT
AAAACAGGGTGTCTCTGCTTCTGCTTCCATAAGAAGAAATGGAGAAAATATATATATATATATATATATTGT
GAAAGATCAATCCATCTGCCAGAACTAGTGGGATGGAAGTTTTTGTACATGTTATCCACCCAGGCCAGGTGGAAG
TAACCTGAATATTTTTTAAATTAAGCAGTTCTACTCAATCACCAGATGCTTCTGAAAATTGCATTTTATACCATTT
CAAATATTTTTTAAAAATAAATACAGTTAACATAGAGTGGTTTCTTATTATGTGAAAATTATTAGCCAGCACCAG
ATGCATGAGCTAATATCTCTTTGAGTCTTCTGCTTCTGTTTGTCTCACAGTAAACTCATTGTTTAAAGCTTCAAGAAC
ATTCAGCTGTTGGTGTGTTAAAAATGCATTGTATTGATTTGACTGGTAGTTTATGAAATTAATTAACACAGG
CCATGAATGGAAGGTGGTATTGCACAGCTAATAAATATGATTTGTGGATATGAA

FIGURE 72

MMVRRGLLAWISRVVLLVLLCCAISVLYMLACTPKGDEEQLALPRANSPTGKEGYQAVLQEW
EQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADLLAFLHSQVDK
AEVNAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPEEKPVKDKRDELVEAIESALETNNPA
ENSPNHRPYTASDFIEGIYRTERDKGTLIELTFKGDHKHEFKRLILFRPFSPIMKVNEKLNMAN
TLINVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGKEEINEVKGILENTSKAANFRNF
TFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTCRLNTQPGKKVFYPVLF
NPGIYGHHDVPPLEQQLVIKKEGTFWRDFGFGMTCQYRSDFINIGGFDDIKGWGGEDVHLYR
KYLHSNLIVVRTPVRLFWHEKRCMDLTPQYKMCMSKAMNEASHGQLGMLVFRHEIEAHL
RKQKQKTSSKKT

Important features:

Signal peptide:

amino acids 1-27

N-glycosylation sites.

amino acids 315-319, 324-328

N-myristoylation sites.

amino acids 96-102, 136-142, 212-218, 311-317, 339-345, 393-399

Amidation site.

amino acids 377-381

CACAGCCCAAGAGGCA

[illegible]

FIGURE 74

MLFSALLLEVIWILAADGGQHWTYEGPHGQDHPASYPECGNAQSPIDIQTDSVTFDPLPALQ
PHGYDQPGTEPLDLHNNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPPGGSEHQINSEAT
FAELHIVHYDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQKTSVPP
FNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTLFSTEEEPSKLLV
QNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVGCLCLLLAVYFIARKIRKKRLENRKS
VVFTSAQATTEA

Important features of the protein:

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 291-310

N-glycosylation site.

amino acids 213-216

Eukaryotic-type carbonic anhydrases proteins

amino acids 197-245, 104-140, 22-69

FIGURE 75

TGCCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGGCGCCTTGGGGACGGGCAGTTCCCTGTGTC
TCTGGTGGTTTGCCATAACCTGCAAACATCACCTTCTTATCCATCAACATGAAGAATGTCCTACA
ATGGACTCCACCAGAGGGTCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATTTTCATCACAA
ATTGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGTCCTGACAGTCC
AGAGAAGTGGAAGAGAAATCCAGAAGACCTTCCTGTTTCCATGCAACAAATATACTCCAATCTGA
AGTATAACGTGTCTGTGTTGAATACTAAATCAAACAGAACGTGGTCCCAGTGTGTGACCAACCAC
ACGCTGGTGCTCACCTGGCTGGAGCCGAACACTCTTTACTGCGTACACGTGGAGTCCCTTCGTCCT
AGGGCCCCCTCGCCGTGCTCAGCCTTCTGAGAAGCAGTGTGCCAGGACTTTGAAAGATCAATCAT
CAGAGTTCAAGGCTAAATCATCTTCTGGTATGTTTTGCCCATATCTATTACCGTGTTCCTTTTT
TCTGTGATGGGCTATTCCATCTACCGATATATCCACGTTGGCAAAGAGAAACCCAGCAAATTT
GATTTTGATTTATGGAATGAATTTGACAAAAGATTCTTTGTGCCTGCTGAAAAATCGTGATTA
ACTTTATCACCTCAATATCTCGGATGATTCTAAAATTTCTCATCAGGATATGAGTTTACTGGGA
AAAAGCAGTGATGTATCCAGCCTTAATGATCCTCAGCCCAGCGGGAACCTGAGGCCCCCTCAGGA
GGAAGAGGAGGTGAAACATTTAGGGTATGCTTCGCATTTGATGGAAATTTTTTGTGACTCTGAAG
AAAACACGGAAGGTACTTCTCTCACCCAGCAAGAGTCCCTCAGCAGAACAAATACCCCGGATAAA
ACAGTCATTGAATATGAATATGATGTCAGAACCACTGACATTTGTGCGGGGCTGAAGAGCAGGA
GCTCAGTTTGAGGAGGAGGTGTCCACACAAGGAACATTATTGGAGTCGCAGGCAGCGTTGGCAG
TCTTGGGCCCCGAAACGTTACAGTACTCATAACCCCTCAGCTCCAAGACTTAGACCCCTGGCG
CAGGAGCACACAGACTCGGAGGAGGGGCCGAGGAAGAGCCATCGACGACCCCTGGTCGACTGGGA
TCCCCAACTGGCAGGCTGTGTATTCCCTTCGCTGTCCAGCTTCGACCAGGATTAGAGGGCTGCG
AGCCTTCTGAGGGGGATGGGCTCGGAGAGGAGGGTCTTCTATCTAGACTCTATGAGGAGCCGGCT
CCAGACAGGCCACCAGGAGAAATGAAACCTATCTCATGCAATTCATGGAGGAATGGGGTTATA
TGTGCAGATGAAAACTGATGCCAACACTTCCTTTTGCTTTTGTTCCTGTGCAACAAGTGAG
TCACCCCTTTGATCCCAGCCATAAAGTACCTGGGATGAAAGAAGTTTTTCCAGTTTGTCACTGT
CTGTGAGAATTACTTATTTCTTTTCTCTATTCTCATAGCACGTGTGTGATTGGTTCATGCATGTA
GGTCTCTTAACAATGATGGTGGGCTCTGGAGTCCAGGGGCTGGCCGGTTGTCTATGCAGAGAA
AGCAGTCAATAAATGTTTGCCAGACTGGGTGCAGAATTTATTCAGGTGGGTGT

FIGURE 76

MSYNGLHQRVFKELKLLTLCSSISQIGPPEVALTTDEKSIISVVLTAPEKWKRNPEDLPVSMQQIY
 SNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSEKQCARTLK
 DQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRYIHVGKEKHPANLILYGNFDRFFVPAEK
 IVINFITLNISSDDSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEEEVKHLGYASHLMEIFC
 DSEENTEGTSLTQQESLSRTIPDPKTVIEYEDVRTTDICAGPEEQELSLQEEVSTQGTLLSQA
 ALAVLGPQTLQYSYTPQLQDLPLAQEHTDSEEGPEEEPSTTLVDWDPQTGRLCIPSLSSFDQDS
 EGCEPSEGDGLGEEGLLSRLYEEPAPDRPPGENETYLMQFMEEWGLYVQMEN

Important features:

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 140-163

N-glycosylation sites.

amino acids 71-74, 80-83, 89-92, 204-207, 423-426

FIGURE 77

GAGGAGCGGGCCGAGGACTCCAGCGTGCCAGGTCTGGCATCCTGCACTTGCTGCCCTCTGACAC
 CTGGGAAGATGGCCGGCCCGTGACCTTCACCCCTTCTCTGTGGTTTGCTGGCAGCCACCTTGATC
 CAAGCCACCCTCAGTCCCCTGACAGTTCTCATCCTCGGCCAAAAGTCATCAAAGAAAAGCTGAC
 ACAGGAGCTGAAGGACCACAACGCCACCAGCATCCTGCAGCAGCTGCCGCTGCTCAGTGCCATGC
 GGGAAAAGCCAGCCGGAGGCATCCCTGTGCTGGGCAGCCTGGTGAACACCGTCCTGAAGCACATC
 ATCTGGCTGAAGGTCATCACAGCTAACATCCTCCAGCTGCAGGTGAAGCCCTCGGCCAATGACCA
 GGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCAACACGCCCTGGTCAAGACCA
 TCGTGGAGTTCCACATGACGACTGAGGCCCAAGCCACCATCCGCATGGACACCAGTGCAAGTGGC
 CCCACCCGCTGGTCCTCAGTGACTGTGCCACCAGCCATGGGAGCCTGCGCATCCAATGCTGTA
 TAAGCTCTCCTTCTGGTGAACGCCTTAGCTAAGCAGGTCATGAACCTCCTAGTGCCATCCCTGC
 CCAATCTAGTGAAAAACCAGCTGTGTCCCGTGATCGAGGCTTCCTTCAATGGCATGTATGCAGAC
 CTCCTGCAGCTGGTGAAGGTGCCCATTTCCCTCAGCATTGACCGTCTGGAGTTTGACCTTCTGTA
 TCCTGCCATCAAGGGTGACACCATTAGCTCTACCTGGGGGCCAAGTTGTTGGACTCACAGGGAA
 AGGTGACCAAGTGGTTCAATAACTCTGCAGCTTCCTTGACAATGCCACCCTGGACAACATCCCCG
 TTCAGCCTCATCGTGAGTCAGGACGTGGTGAAAGCTGCAGTGGCTGCTGTGCTCTCTCCAGAAGA
 ATTCATGGTCCTGTTGGACTCTGTGCTTCCTGAGAGTGCCCATCGGCTGAAGTCAAGCATCGGGC
 TGATCAATGAAAAGGCTGCAGATAAGCTGGGATCTACCCAGATCGTGAAGATCCTAACTCAGGAC
 ACTCCCAGATTTTTTATAGACCAAGGCCATGCCAAGGTGGCCCAACTGATCGTGCTGGAAGTGTT
 TCCCTCCAGTGAAGCCCTCCGCCCTTTGTTACCCCTGGGCATCGAAGCCAGCTCGGAAGCTCAGT
 TTTACACCAAAGGTGACCAACTTATACTCAACTTGAATAACATCAGCTCTGATCGGATCCAGCTG
 ATGAACTCTGGGATTGGCTGGTTCCAACCTGATGTTCTGAAAAACATCATCACTGAGATCATCCA
 CTCCATCCTGCTGCCGAACCAGAATGGCAAATTAAGATCTGGGGTCCCAGTGTCATTGGTGAAGG
 CCTTGGGATTCGAGGCAGCTGAGTCCTCACTGACCAAGGATGCCCTTGTGCTTACTCCAGCCTCC
 TTGTGGAAACCCAGCTCTCCTGTCTCCAGTGAAGACTTGATGGCAGCCATCAGGGAAGGCTGG
 GTCCCAGCTGGGAGTATGGGTGTGAGCTCTATAGACCATCCCTCTCTGCAATCAATAAACACTTG
 CCTGTGAAAAA

FIGURE 78

MAGPWTFTLLCGLLAATLIQATLSPTAVLIIGPKVIKEKLTQELKDHNATSILQQLPLLSAMREK
PAGGIPVLGSLVNTVLKHIIWLKVITANILQLQVKPSANDQELLVKIPLDMVAGFNTPLVKTIIVE
FHMTTEAQATIRMDTSASGPTRLVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMNLLVPSLPNL
VKNQLCPVIEASFNGMYADLLQLVKVPISLSIDRLEFDLLYPAIKGDTIQLYLGAKLKLDSSQKVT
KWFNNSAASLTMPITLDNIPFSLIVSQDVVKAAVAVALSPPEEFMVLLDSVLPESAHLKSSIGLIN
EKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSSSEALRPLFTLGIEASSEAQFYT
KGDQLILNLNNISSDRIQLMNSGIGWFQPDVLKNIITEIIHSILLPNQNGKLRSGVPVSLVKALG
FEAAESSLTKDALVLTPASLWKPSSPVSQ

Important features of the protein:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 48-51, 264-267, 401-404

Glycosaminoglycan attachment site.

amino acids 412-415

LBP / BPI / CETP family proteins.

amino acids 407-457

FIGURE 79

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAGAGC
TTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCCATGGCCTCT
CTTGGCCTCCAACCTTGTTGGGCTACATCCTAGGCCTTCTGGGGCTTTGGGCACACTGGTTGCCAT
GCTGCTCCCCAGCTGGAAAACAAGTTCTTATGTGGTGCCAGCATTGTGACAGCAGTTGGCTTCT
CCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCATCACCCAGTGTGACATCTATAGC
ACCCCTTCTGGGCCTGCCCCTGACATCCAGGCTGCCCAGGCCATGATGGTGACATCCAGTGCAAT
CTCCTCCCTGGCCTGCATTATCTCTGTGGTGGGCATGAGATGCACAGTCTTCTGCCAGGAATCCC
GAGCCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTTTCATCCTTGGAGGCCTCCTGGGATTC
ATTCTGTGGCCTGGAATCTTTCATGGGATCTACGGGACTTCTACTCACCACCTGGTGCCTGACAG
CATGAAATTTGAGATTGGAGAGGCTCTTTACTTGGGCATTATTTCTTCCCTGTTCTCCCTGATAG
CTGGAATCATCCTCTGCTTTTCTGCTCATCCCAGAGAAATCGCTCCAACCTACTACGATGCCTAC
CAAGCCCAACCTCTTGCCACAAGGAGCTCTCCAAGGCCTGGTCAACCTCCCAAAGTCAAGAGTGA
GTTCAATTCTACAGCCTGACAGGGTATGTGTGAAGAACCAGGGGCCAGAGCTGGGGGGTGGCTG
GGTCTGTGAAAAACAGTGGACAGCACCCCGAGGGCCACAGGTGAGGGACACTACCCTGGATCGT
GTCAGAAGGTGCTGCTGAGGATAGACTGACTTTGGCCATTGGATTGAGCAAAGGCAGAAATGGGG
GCTAGTGTAAACAGCATGCAGGTTGAATTGCCAAGGATGCTCGCCATGCCAGCCTTTCTGTTTTCC
TCACCTTGCTGCTCCCCTGCCCTAAGTCCCCAACCCCTCAACTTGAAACCCCATTCCTTAAGCCA
GGACTCAGAGGATCCCTTTGCCCTCTGGTTTACCTGGGACTCCATCCCCAAACCCACTAATCACA
TCCCCTGACTGACCCTCTGTGATCAAAGACCCCTCTCTCTGGCTGAGGTTGGCTCTTAGCTCATT
GCTGGGGATGGGAAGGAGAAGCAGTGGCTTTTGTGGGCATTGCTCTAACCTACTTCTCAAGCTTC
CCTCCAAAGAACTGATTGGCCCTGGAACCTCCATCCCCTCTTGTATGACTCCACAGTGTCCA
GACTAATTTGTGCATGAACTGAAATAAAACCATCTACGGTATCCAGGGAACAGAAAGCAGGATG
CAGGATGGGAGGACAGGAAGGCAGCCTGGGACATTTAAAAAATA

[Faint, illegible handwritten notes]

Important features of the protein:

amino acids 1-24

amino acids 82-102, 117-140, 163-182

amino acids 190-193

amino acids 46-59

FIGURE 81

CCCACGCGTCCGCGCCTCTCCCTTCTGCTGGACCTTCCTTCGTCTCTCCATCTCTCCCTCCTTTC
 CCCGCGTTCTCTTTCCACCTTTCTCTTCTTCCCACCTTAGACCTCCCTTCCTGCCCTCCTTTCTCT
 GCCCACCGCTGCTTCCTGGCCCTTCTCCGACCCGCTCTAGCAGCAGACCTCCTGGGGTCTGTGG
 GTTGATCTGTGGCCCTGTGCCTCCGTGTCTTTTCGTCTCCCTTCCTCCCGACTCCGCTCCCGG
 ACCAGCGGCCTGACCCTGGGGAAAGGATGGTTCCCAGAGTGAGGGTCTCTCCTCCTTGCTGGGA
 CTCGCGCTGCTCTGGTTCCCCCTGGACTCCCACGCTCGAGCCCGCCAGACATGTTCTGCCTTTT
 CCATGGGAAGAGATACTCCCCGGCGAGAGCTGGCACCCCTACTTGGAGCCACAAGGCCTGATGT
 ACTGCCTGCGCTGTACCTGCTCAGAGGGCGCCCATGTGAGTTGTTACCGCCTCCACTGTCCGCCT
 GTCCACTGCCCCAGCCTGTGACGGAGCCACAGCAATGCTGTCCAAGTGTGTGGAACCTCACAC
 TCCCTCTGGACTCCGGGCCCCACCAAAGTCTGCCAGCACAAACGGGACCATGTACCAACACGGAG
 AGATCTTCAGTGCCCATGAGCTGTTCCCTCCCGCCTGCCCAACCAGTGTGTCCTCTGCAGCTGC
 ACAGAGGGCCAGATCTACTGCGGCCTCACAACCTGCCCGAACCAGGCTGCCAGCACCCCTCCC
 ACTGCCAGACTCCTGCTGCCAAGCCTGCAAAGATGAGGCAAGTGAGCAATCGGATGAAGAGGACA
 GTGTGCAGTCGCTCCATGGGGTGAGACATCCTCAGGATCCATGTTCCAGTGATGCTGGGAGAAAG
 AGAGGGCCGGGCACCCAGCCCCACTGGCCTCAGCGCCCTCTGAGCTTCATCCCTCGCCACTT
 CAGACCCAAGGGAGCAGGCAGCACAACTGTCAAGATCGTCCTGAAGGAGAAACATAAGAAAGCCT
 GTGTGCATGGCGGGAAGACGTACTCCACGGGGAGGTGTGGCACCCGGCCTTCCGTGCCTTCGGC
 CCCTTGCCCTGCATCCTATGCACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCC
 CACCGAGTACCCCTGCCGTCAACCCGAGAAAGTGCTGGGAAGTGCTGCAAGATTTGCCAGAGG
 ACAAGCAGACCCTGGCCACAGTGAGATCAGTTCTACCAGGTGTCCAAGGCACCGGGCCGGGTCT
 CTCGTCCACACATCGGTATCCCCAAGCCCAGACAACCTGCGTCGCTTTGCCCTGGAACACGAGGC
 CTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGGTAAAAGATGAGGAACTGAGGCTCAGAGAG
 GTGAAGTACCTGGCCCAAGGCCACACAGCCAGAATCTTCCACTTGACTCAGATCAAGAAAGTCAG
 GAAGCAAGACTTCCAGAAAGAGGCACAGCACTTCCGACTGCTCGCTGGCCCCACGAAGGTCACT
 GGAACGTCTTCTAGCCCAGACCCTGGAGCTGAAGGTCACGGCCAGTCCAGACAAAGTGACCAAG
 ACATAACAAAGACC**TAA**CAGTTGCAGATATGAGCTGTATAATTGTTGTTATTATATATTAATAAA
 TAAGAAGTTGCATTACCCTCAAAAAAAAAAAAAAAAAAAAAA

FIGURE 82

MVPEVRVLSSLLGLALLWFPLDSHARARPDMFCLFHGKRYSPGESWHPYLEPQGLMYCLRCTCSE
GAHVSCYRLHCPPVHCPQPVTEPQQCCPKCVEPHTPSGLRAPPKSCQHNGTMYQHGEIFSAHEL
PSRLPNQCVLCSCTEGQIYCGLTTCPEPGCPAPLPLPDSCCQACKDEASEQSDEEDSVQSLHGVR
HPQDPCSSDAGRKRGPPTAPTGLSAPLSFIPRHFRPKGAGSTTVKIVLKEKHKKACVHGGKTY
HGEVWHPAFRAFGPLPCILCTCEDGRQDCQRVTCPTCYPCRHPKAGKCKICPEDKADPGHSE
ISSTRCPKAPGRVLVHTSVSPSPDNLRRFALEHEASDLVEIYLWKLVKDEETEAQRGEVPGPRPH
SQNLPLDSDQESQEARLPERGTALPTARWPFRSLERLPSDPGAEGHGQSRQSDQDITKT

Signal peptide:
amino acids 1-25

FIGURE 84

MALMLSLVLSLLKLGSGQWQVFGPDKPVQALVGEDAAFSCFLSPKTNAEAMEVRFFRGQFSSVVH
LYRDGKDQPFMQMPQYQGRTKLVKDSIAEGRISLRLENITVLDAGLYGCRISSQSYQKAIWELQ
VSALGSVPLISITGYVDRDIQLLCQSSGWFPRTAKWKGPQGQDLSTDSRTNRDMHGLFDVEISL
TVQENAGSISCSMRHAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLFFGIVGLKIFFSK
FQWKIQAELDWRRKHGQAEIRDARKHAVEVTLPETAHPKLCVSDLKTVTHRKAQEVPHSEKRF
TRKSVVASQSFQAGKHYWEVDGGHNKRWRVGVCRDDVDRRKEYVTLSPDHGYWVLRNLNGEHLFT
LNPRFISVFPRTPTTKIGVFLDYECGTISFFNINDQSLIYTLTCRFEGLLRPYIEYPSYNEQNGT
PIVICPVTQESEKEASWQRASAIPESTSNESSQATTFFLPRGEM

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 239-255

$$\frac{d}{dt} \left(\frac{\partial L}{\partial \dot{x}} \right) = \frac{\partial L}{\partial x}, \quad \frac{d}{dt} \left(\frac{\partial L}{\partial \dot{y}} \right) = \frac{\partial L}{\partial y}$$

APP ID=10063520

FIGURE 86

MLLLLLPLLWGRERAEGQTSKLLTMQSSVTVQEGLCVHVPCSFSYPSHGWIIYPGPVVHGYWFREG
 ANTDDQDAPVATNNPARAVWEETRDRFHLLGDPHTKNCTLSIRDARRSDAGRYFFRMEKGSIKWNY
 KHHRLSVNVTALTHRPNILIPGTLESGCPQNLTCVSPWACEQGTTPPMISWIGTSVSPLDPSTTRS
 SVLTLIPQPQDHGTSLTCQVTFFGASVTTNKTVHLNVSYPQNLMTVFQGDGTVSTVLGNGSSL
 SLPEGQSLRLVCAVDAVDSNPPARLSLSWRGLTLCPSQPSNPGVLELPWVHLRDAAEFTCRAQNP
 LGSQQVYLVNLSQSKATSGVTQGVVGGAGATALVFLSFCVIFVVVRSCRKKSARPAAGVGDGTGIE
 DANAVRGASASQGPLTEPWAEDSPPDQPPASARSSVGEGELQYASLSFQMVKPWDSRGQEATDTE
 YSEIKIHR

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 351-370

FIGURE 87

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGGAGGGAGGGAGTGAAGGAGCTCTCTGTAC
CCAAGGAAAGTGCAGCTGAGACTCAGACAAGATTACAATGAACCAACTCAGCTTCCTGCTGTTTC
TCATAGCGACCACCAGAGGATGGAGTACAGATGAGGCTAATACTTACTTCAAGGAATGGACCTGT
TCTTCGTCTCCATCTCTGCCCAGAAGCTGCAAGGAAATCAAAGACGAATGTCTTAGTGCATTTGA
TGGCCTGTATTTTCTCCGCACTGAGAATGGTGTATCTACCAGACCTTCTGTGACATGACCTCTG
GGGGTGGCGGCTGGACCCTGGTGGCCAGCGTGCATGAGAATGACATGCGTGGGAAGTGCACGGTG
GGCGATCGCTGGTCCAGTCAGCAGGGCAGCAAAGCAGACTACCCAGAGGGGGACGGCAACTGGGC
CAACTACAACACCTTTGGATCTGCAGAGGCGGCCACGAGCGATGACTACAAGAACCCTGGCTACT
ACGACATCCAGGCCAAGGACCTGGGCATCTGGCACGTGCCAATAAGTCCCCCATGCAGCACTGG
AGAAACAGCTCCCTGCTGAGGTACCGCACGGACACTGGCTTCCTCCAGACACTGGGACATAATCT
GTTTGGCATCTACCAGAAATATCCAGTGAAATATGGAGAAGGAAAGTGTGGACTGACAACGGCC
CGGTGATCCCTGTGGTCTATGATTTTGGCGACGCCAGAAAACAGCATCTTATTACTCACCTAT
GGCCAGCGGGAATTCAGTGCGGGATTTGTTTCAGTTCAGGGTATTTAATAACGAGAGAGCAGCCAA
CGCCTTGTGTGCTGGAATGAGGGTCACCGGATGTAACACTGAGCATCACTGCATTGGTGGAGGAG
GATACTTTCCAGAGGCCAGTCCCCAGCAGTGTGGAGATTTTCTGGTTTTGATTGGAGTGGATAT
GGAACATCATGTTGGTTACAGCAGCAGCCGTGAGATAACTGAGGCAGCTGTGCTTCTATTCTATCG
TTGAGAGTTTTTGTGGGAGGGAACCCAGACCTCTCCTCCCAACCATGAGATCCCAAGGATGGAGAA
CAACTTACCCAGTAGCTAGAATGTTAATGGCAGAAGAGAAAACAATAAATCATATTGACTCAAGA
AAAAAA

[illegible]

Important features:

amino acids 1-16

amino acids 163-167

amino acids 74-78, 289-293

amino acids 76-82, 115-121, 124-130, 253-259, 292-298

FIGURE 89

CTAGATTTGTCGGCTTGCAGGGAGACTTCAGGAGTCGCTGTCTCTGAACTTCCAGCCTCAGAGAC
CGCCGCCCTTGTCCCGAGGGCCATGGCCGGGTCTCAGGGCTTGTGCCCTCTCGCTTCCTGACG
CTCCTGGCGCATCTGGTGGTCGTCATCACCTTATTCTGGTCCCGGGACAGCAACATACAGGCCTG
CCTGCCTCTCACGTTACCCCCGAGGAGTATGACAAGCAGGACATTTCAGCTGGTGGCCGCGCTCT
CTGTCACCCTGGGCCTCTTTGCAGTGGAGCTGGCCGGTTTCCTCTCAGGAGTCTCCATGTTCAAC
AGCACCCAGAGCCTCATCTCCATTGGGGCTCACTGTAGTGCATCCGTGGCCCTGTCTTCTTCAT
ATTCGAGCGTTGGGAGTGCCTACGTATTGGTACATTTTTGTCTTCTGCAGTGGCCCTTCAGCTG
TCACTGAAATGGCTTTATTCGTCACCGTCTTTGGGCTGAAAAAGAAACCCTTCTGATTACCTTCA
TGACGGGAACCTAAGGACGAAGCCTACAGGGGCAAGGGCCGCTTCGTATTCTGGAAGAAGGAAG
GCATAGGCTTCGGTTTTCCCTCGGAACTGCTTCTGCTGGAGGATATGTGTTGGAATAATTACG
TCTTGAGTCTGGGATTATCCGCATTGTATTTAGTGCTTTGTAATAAAATATGTTTTGTAGTAACA
TTAAGACTTATATACAGTTTTAGGGGACAATTAAAAAAAAAAAA

FIGURE 90

MGRVSGLVPSRFLTLLAHLVVITLFWSRDSNIQACPLTFTPEEYDKQDIQLVAALSVTLGLFA
VELAGFLSGVSMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFCALPAVTEMALFV
TVFGLKKKPF

Transmembrane domain:

amino acids 12-28 (type II), 51-66, 107-124

FIGURE 91

CTGGGACCCCCGAAAAGAGAAGGGGAGAGCGAGGGGACGAGAGCGGAGGAGGAAGATGCAACTGAC
TCGCTGCTGCTTCGTGTTCCCTGGTGCAGGGTAGCCTCTATCTGGTCATCTGTGGCCAGGATGATG
GTCTCCCCGGCTCAGAGGACCCTGAGCGTGATGACCACGAGGGCCAGCCCCGGCCCCGGGTGCCT
CGGAAGCGGGGCCACATCTCACCTAAGTCCCGCCCCATGGCCAATTCCTACTCTCTAGGGCTGCT
GGCCCCGCCTGGGGAGGCTTGGGGCATTCTTGGGCAGCCCCCAACCGCCCGAACCACAGCCCCC
CACCTCAGCCAAGGTGAAGAAAATCTTTGGCTGGGGCGACTTCTACTCCAACATCAAGACGGTG
GCCCTGAACCTGCTCGTCACAGGGAAGATTGTGGACCATGGCAATGGGACCTTCAGCGTCCACTT
CCAACACAATGCCACAGGCCAGGGAACATCTCCATCAGCCTCGTGCCCCCAGTAAAGCTGTAG
AGTTCACCAGGAACAGCAGATCTTCATCGAAGCCAAGGCCTCCAAAATCTTCAACTGCCGGATG
GAGTGGGAGAAGGTAGAACGGGGCCCGCGGACCTCGCTTTGCACCCACGACCCAGCCAAGATCTG
CTCCCGAGACCACGCTCAGAGCTCAGCCACCTGGAGCTGCTCCAGCCCTTCAAAGTCGTCTGTG
TCTACATCGCCTTCTACAGCACGGACTATCGGCTGGTCCAGAAGGTGTGCCCAGATTACAACATC
CATAGTGATACCCCTACTACCATCTGGGTGACCCGGGGCAGGCCACAGAGGCCAGGCCAGGGC
TGGAAGGACAGGCCTGCCCATGCAGGAGACCATCTGGACACCGGGCAGGGAAGGGGTGGGCCTC
AGGCAGGGAGGGGGTGGAGACGAGGAGATGCCAAGTGGGGCCAGGGCCAAGTCTCAAGTGGCAG
AGAAAGGGTCCCAAGTGCTGGTCCCAACCTGAAGCTGTGGAGTGACTAGATCACAGGAGCACTGG
AGGAGGAGTGGGCTCTCTGTGCAGCCTCACAGGGCTTTGCCACGGAGCCACAGAGAGATGCTGGG
TCCCCGAGGCCTGTGGGCAGGCCGATCAGTGTGGCCCCAGATCAAGTCATGGGAGGAAGCTAAGC
CCTTGTTCTTGCCATCCTGAGGAAAGATAGCAACAGGGAGGGGGAGATTCATCAGTGTGGACA
GCCTGTCAACTTAGGATGGATGGCTGAGAGGGCTTCCTAGGAGCCAGTCAGCAGGGTGGGGTGGG
GCCAGAGGAGCTCTCCAGCCCTGCCTAGTGGGCGCCCTGAGCCCCCTGTCTGTGTGCTGAGCATGG
CATGAGGCTGAAGTGGAACCCCTGGGGTCTTTGATGTCTTGACAGATTGACCATCTGTCTCCAGC
CAGGCCACCCCTTTCCAAAATTCCTCTTCTGCCAGTACTCCCCCTGTACCACCCATTGTGTGATG
GCACACCCATCCTTAAGCTAAGACAGGACGATTGTGGTCTCCACACTAAGGCCACAGCCCATC
CGCGTGCTGTGTGTCCCTCTTCCACCCCAACCCCTGCTGGCTCCTCTGGGAGCATCCATGTCCCCG
GAGAGGGGTCCCTCAACAGTCAGCCTCACCTGTGACACGGGGTCTCCCGGATCTGGATGGCGC
CGCCCTCTCAGCAGCGGGCACGGGTGGGGCGGGGCCGCGCAGAGCATGTGCTGGATCTGTTC
TGTGTGTCTGTCTGTGGGTGGGGGAGGGGAGGGAAGTCTTGTGAAACCGCTGATTGCTGACTTT
TGTGTGAAGAATCGTGTCTTGGAGCAGGAATAAAGCTTGCCCCGGGGCA

FIGURE 92

MQLTRCCFVFLVQGSLYLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMANSTL
LGLLAPPGEAWGILGQPPNRPNHSPPSAKVKKIFGWGDFYSNIKTVALNLLVTGKIVDHGNGTF
SVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMWEKVERGRRTSLCTHDP
AKICSRDHAQSSATWSCSQPFKVVCVYIAFYSTDYRLVQKVC PDYNYHSDTPYYPSG

Important features of the protein:

Signal peptide:

amino acids 1-14

N-glycosylation sites.

amino acids 62-65, 127-130, 137-140, 143-146

2-oxo acid dehydrogenases acyltransferase

amino acids 61-71

FIGURE 93

CGGTGGCCATGACTGCGGCCGTGTTCTTCGGCTGCGCCTTCATTGCCTTCGGGGCCTGCGCTCGCC
CTTTATGTCTTCACCATCGCCATCGAGCCGTGCGTATCATCTTCCTCATCGCCGGAGCTTTCTT
CTGGTTGGTGTCTCTACTGATTCGTCCCTTGTTTGGTTCATGGCAAGAGTCATTATTGACAACA
AAGATGGACCAACACAGAAATATCTGCTGATCTTTGGAGCGTTTGTCTCTGTCTATATCCAAGAA
ATGTTCCGATTTGCATATTATAAACTCTTAAAAAAGCCAGTGAAGGTTTGAAGAGTATAAACCC
AGGTGAGACAGCACCCCTCTATGCGACTGCTGGCCTATGTTTCTGGCTTGGGCTTTGGAATCATGA
GTGGAGTATTTTCCTTTGTGAATACCCTATCTGACTCCTTGGGGCCAGGCACAGTGGGCATTTCAT
GGAGATTCTCCTCAATTCTTCCTTTATTTCAGCTTTTCATGACGCTGGTCATTATCTTGCTGCATGT
ATTCTGGGGCATTGTATTTTTTTGATGGCTGTGAGAAGAAAAAGTGGGGCATCCTCCTTATCGTTC
TCCTGACCCACCTGCTGGTGTGAGCCAGACCTTCATAAGTTCTTATTATGGAATAAACCTGGCG
TCAGCATTTATAATCCTGGTGCTCATGGGCACCTGGGCATTCTTAGCTGCGGGAGGCAGCTGCCG
AAGCCTGAAACTCTGCCTGCTCTGCCAAGACAAGAACTTTCTTCTTTACAACCAGCGCTCCAGAT
AACCTCAGGGAACCAGCACTTCCCAAACCGCAGACTACATCTTTAGAGGAAGCACAACTGTGCCT
TTTTCTGAAAATCCCTTTTCTGGTGGAATTGAGAAAGAAATAAACTATGCAGATA

FIGURE 94

MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISLVWFMARVIIDNKDG
PTQKYLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGLGFGIMSGV
FSFVNTLSDSLGPSTVGIHGDSPOFFLYSAFMTLVIILLHVFWGIVFFDGCEKKKGILLIVLLT
HLLVSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSCLKCLLCQDKNFFLYNQSR

Important features of the protein:

Signal peptide:

amino acids 1-19

Transmembrane domains:

amino acids 32-51, 119-138, 152-169, 216-235

Glycosaminoglycan attachment site.

amino acids 120-123

Sodium:neurotransmitter symporter family protein

amino acids 31-65

FIGURE 95

AATTTTTCACCAGAGTAACTTGAGAAACCAACTGGACCTTGAGTATTGTACATTTTGCCTCGTG
 GACCCAAAGGTAGCAATCTGAAACATGAGGAGTACGATTCTACTGTTTGTCTTCTAGGATCAAC
 TCGGTCATTACCACAGCTCAAACCTGCTTTGGGACTCCCTCCCACAAAAGTGGCTCCGGATCAGG
 GAACACTACCAAACCAACAGCAGTCAAATCAGGTCTTTCCTTCTTTAAGTCTGATACCATTAACA
 CAGATGCTCACACTGGGGCCAGATCTGCATCTGTAAATCCTGCTGCAGGAATGACACCTGGTAC
 CCAGACCCACCCATTGACCCTGGGAGGGTTGAATGTACAACAGCAACTGCACCCACATGTGTTAC
 CAATTTTGTGCACACAACCTGGAGCCCAGGGCACTATCCTAAGCTCAGAGGAATTGCCACAAATC
 TTCACGAGCCTCATCATCCATTCCCTTGTTCCCGGAGGCATCCTGCCCACCAGTCAGGCAGGGGC
 TAATCCAGATGTCCAGGATGGAAGCCTTCCAGCAGGAGGAGCAGGTGTAAATCCTGCCACCCAGG
 GAACCCAGCAGGCCCGCTCCCAACTCCCAGTGGCACAGATGACGACTTTGCAGTGACCACCCCT
 GCAGGCATCCAAAGGAGCACACATGCCATCGAGGAAGCCACCACAGAATCAGCAAATGGAATTCA
 GTAAGCTGTTTCAAATTTTTTCAACTAAGCTGCCTCGAATTTGGTGATACATGTGAATCTTTATC
 ATTGATTATATTATGGAATAGATTGAGACACATTGGATAGTCTTAGAAGAAATTAATTCTTAATT
 TACCTGAAAATATTCTTGAAATTTTCAGAAAATATGTTCTATGTAGAGAATCCCAACTTTTAAAAA
 CAATAATTCAATGGATAAATCTGTCTTTGAAATATAACATTATGCTGCCTGGATGATATGCATAT
 TAAACATATTTGGAAAAGTGGAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 96

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQQSNOVFPSLSLIPLTQM
LTLGPDHLHLLNPAAGMTPGTQTHPLTLGGLNVQQQLHHPVLPPIFVTQLGAQGTILSSEE
LPQIFTSLIIHSLFPGGILPTSQAGANPDVQDGSLPAGGAGVNPATQGTGAGRLPTPSG
TDDDFAVTTPAGIQRSTHAIEEATTESANGIQ

Signal peptide:
amino acids 1-16

FIGURE 97

GCTCAAGTGCCCTGCCTTGCCCCACCCAGCCAGCCTGGCCAGAGCCCCCTGGAGAAGGAGCTCT
CTTCTTGCTTGGCAGCTGGACCAAGGGAGCCAGTCTTGGGCGCTGGAGGGCTGTCTTGACCATG
GTCCCTGCCTGGCTGTGGCTGCTTTGTGTCTCCGTCCCCCAGGCTCTCCCCAAGGCCAGCCTGC
AGAGCTGTCTGTGAAGTTCCAGAAAATATGGTGGAAATTTCCCTTTATACCTGACCAAGTTGC
CGCTGCCCCGTGAGGGGGCTGAAGGCCAGATCGTGCTGTGAGGGGACTCAGGCAAGGCAACTGAG
GGCCCATTTGCTATGGATCCAGATTCTGGCTTCCTGCTGGTGACCAGGGCCCTGGACCCGAGAGGA
GCAGGCAGAGTACCAGCTACAGGTCACCCCTGGAGATGCAGGATGGACATGTCTTGTGGGGTCCAC
AGCCTGTGCTTGTGCACGTGAAGGATGAGAATGACCAGGTGCCCCATTTCTCTCAAGCCATCTAC
AGAGCTCGGCTGAGCCGGGGTACCAGGCCTGGCATCCCCCTTCTCTTCTGAGGCTTCAGACCG
GGATGAGCCAGGCACAGCCAACTCGGATCTTCGATTCCACATCCTGAGCCAGGCTCCAGCCCAGC
CTTCCCCAGACATGTTCAGCTGGAGCCTCGGCTGGGGGCTCTGGCCCTCAGCCCCAAGGGGAGC
ACCAGCCTTGACCACGCCCTGGAGAGGACCTACCAGCTGTTGGTACAGGTCAAGGATGGGTGA
CCAGGCCTCAGGCCACCAGGCCACTGCCACCGTGAAGTCTCCATCATAGAGAGCACCTGGGTGT
CCCTAGAGCCTATCCACCTGGCAGAGAATCTCAAAGTCCATATACCCGCACCATGGCCCAGGTA
CACTGGAGTGGGGGTGATGTGCACTATCACCTGGAGAGCCATCCCCCGGACCCCTTTGAAGTGAA
TGCCAGAGGGAACCTCTACGTGACCAGAGAGCTGGACAGAGAAGCCAGGCTGAGTACCTGCTCC
AGGTGCGGGCTCAGAATTTCCATGGCGAGGACTATGCGGCCCTCTGGAGCTGCACGTGCTGGT
ATGGATGAGAATGACAACGTGCCTATCTGCCCTCCCCGTGACCCACAGTCAGCATCCCTGAGCT
CAGTCCACCAGGTAAGTGAAGTACTGACCTGTCAGCAGAGGATGCAGATGCCCCCGGCTCCCCCA
ATTTCCACGTTGTGATCAGCTCCTGAGCCCTGAGCCTGAGGATGGGGTAGAGGGAGAGCCTTC
CAGGTGGACCCCACTTCAGGCAGTGTGACGCTGGGGGTGCTCCCACTCCGAGCAGGCCAGAACAT
CCTGCTTCTGGTGTGCGCATGGACCTGGCAGGCGCAGAGGGTGGCTTCAGCAGCACGTGTGAAG
TCGAAGTCGCAGTCACAGATATCAATGATCACGCCCTGAGTTCATCACTTCCAGATTGGGCCCT
ATAAGCCTCCCTGAGGATGTGGAGCCCGGACTCTGGTGGCCATGCTAACAGCCATTGATGCTGA
CCTCGAGCCCGCCTTCCGCCTCATGGATTTTGCCATTGAGAGGGGAGACACAGAAGGGACTTTTG
GCCTGGATTGGGAGCCAGACTCTGGGCATGTTAGACTCAGACTCTGCAAGAACCTCAGTTATGAG
GCAGCTCAAGTCATGAGGTGGTGGTGGTGGTGCAGAGTGTGGCGAAGCTGGTGGGGCCAGGCC
AGGCCCTGGAGCCACCGCCACGGTGACTGTGCTAGTGGAGAGAGTGTATGCCACCCCCAAGTTGG
ACCAGGAGAGCTACGAGGCCAGTGTCCCATCAGTGCCCCAGCCGGCTCTTCTGCTGACCATC
CAGCCCTCCGACCCCATCAGCCGAACCCCTCAGGTTCTCCCTAGTCAATGACTCAGAGGGCTGGCT
CTGCATTGAGAAATTTCTCCGGGGAGGTGCACACCGCCAGTCCCTGCAGGGCGCCAGCCTGGGG
ACACCTACACGGTGCTTGTGGAGGCCAGGATACAGCCCTGACTCTTGCCCTGTGCCCTCCCAA
TACCTCTGCACACCCCGCCAAGACCATGGCTTGATCGTGAGTGACCCAGCAAGGACCCCGATCT
GGCCAGTGGGCACGGTCCCTACAGCTTCACCCCTGGTCCCAACCCACGGTGCAACGGGATTGGC
GCCTCCAGACTCTCAATGGTTCCCATGCCTACCTACCTTGGCCCTGCATTGGGTGGAGCCACGT
GAACACATAATCCCCGTGGTGGTCAGCCACAATGCCAGATGTGGCAGCTCCTGGTTCGAGTGAT
CGTGTGTGCTGCAACGTGGAGGGGAGTGATGCGCAAGGTGGGCCGATGAAGGGCATGCCCA
CGAAGCTGTGCGCAGTGGGCATCCTTGTAGGCACCTGGTAGCAATAGGAATCTTCTCATCTCT
ATTTTCAACCCACTGGACCATGTCAAGGAAGAAGGACCCGGATCAACCAGCAGACAGCGTGCCCT
GAAGGCGACTGTCTGAATGGCCCAGGCAGCTCTAGCTGGGAGCTTGGCCTCTGGCTCCATCTGAG
TCCCTTGGGAGAGAGCCAGCACCCAAGATCCAGAGGGGACAGGACAGAGTAGAAGCCCTCCA
TCTGCCCTGGGGTGGAGGCACCATCACCATCACAGGCATGTCTGCAGAGCCTGGACACCAACTT
TATGGACTGCCCATGGGAGTGCTCCAAATGTCAGGGTGTGTTGCCCAATAATAAGCCCGAGAGAA
CTGGGCTGGGCCCTATGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAG

FIGURE 99

GGCTGACCGTGCTACATTGCCTGGAGGAAGCCTAAGGAACCCAGGCATCCAGCTGCCCCACGCCTG
 AGTCCAAGATTCTTCCCAGGAACACAAACGTAGGAGACCCACGCTCCTGGAAGCACCAGCCTTTA
 TCTCTTACACCTTCAAGTCCCCTTTCTCAAGAATCCTCTGTCTTTTGCCCTCTAAAGTCTTGGTAC
 ATCTAGGACCCAGGCATCTTGCTTTCCAGCCACAAAGAGACAGATGAAGATGCAGAAAGGAAATG
 TTCTCCTTATGTTTGGTCTACTATTGCATTAGAAAGCTGCAACAAATCCAATGAGACTAGCACC
 TCTGCCAACACTGGATCCAGTGTGATCTCCAGTGGAGCCAGCACAGCCACCAACTCTGGGTCCAG
 TGTGACCTCCAGTGGGGTCAGCACAGCCACCATCTCAGGGTCCAGCGTGACCTCCAATGGGGTCA
 GCATAGTCAACCACTCTGAGTTCCATACAACCTCCAGTGGGATCAGCACAGCCACCAACTCTGAG
 TTCAGCACAGCGTCCAGTGGGATCAGCATAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGG
 GGCCAGCACAGCCACCAACTCTGAGTCCAGCACACCCTCCAGTGGGGCCAGCACAGTCAACCACT
 CTGGGTCCAGTGTGACCTCCAGTGGAGCCAGCACTGCCACCAACTCTGAGTCCAGCACAGTGTCC
 AGTAGGGCCAGCACTGCCACCAACTCTGAGTCTAGCACACTCTCCAGTGGGGCCAGCACAGCCAC
 CAACTCTGACTCCAGCACAACTCCAGTGGGGCTAGCACAGCCACCAACTCTGAGTCCAGCACAA
 CCTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAGCACT
 GCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAG
 AACGACCTCCAATGGGGCTGGCACAGCCACCAACTCTGAGTCCAGCACAGCTCCAGTGGGGCCA
 GCACAGCCACCAACTCTGACTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAG
 TCCAGCACGACCTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGG
 GGCTAGCACAGCCACCAACTCTGACTCCAGCACAACTCCAGTGGGGCCGGCACAGCCACCAACT
 CTGAGTCCAGCACAGTGTCCAGTGGGATCAGCACAGTCACCAATTCTGAGTCCAGCACACCCCTCC
 AGTGGGGCCAACACAGCCACCAACTCTGAGTCCAGTACGACCTCCAGTGGGGCCAACACAGCCAC
 CAACTCTGAGTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAGTCCAGCACAA
 CCTCCAGTGGGGTCAGCACAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGCTAGCACA
 GCCACCAACTCTGACTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCTAG
 CACAGTGTCCAGTGGGATCAGCACAGTCACCAATTCTGAGTCCAGCACAACTCCAGTGGGGCCA
 ACACAGCCACCAACTCTGGGTCCAGTGTGACCTCTGCAGGCTCTGGAACAGCAGCTCTGACTGGA
 ATGCACACAACTTCCCATAGTGCATCTACTGCAGTGAAGTGAAGCAAAGCCTGGTGGGTCCCTGGT
 GCCGTGGGAAATCTTCTCATCACCTGGTCTCGGTTGTGGCGGCCGTGGGGCTCTTTGCTGGGC
 TCTTCTTCTGTGTGAGAAACAGCCTGTCCCTGAGAAACACCTTTAACACAGTGTCTACACCCCT
 CATGGCCTCAACCATGGCCTTGGTCCAGGCCCTGGAGGGAATCATGGAGCCCCCACAGGCCCAG
 GTGGAGTCCTAACTGGTCTGGAGGAGACCAGTATCATCGATAGCCATGGAGATGAGCGGGAGGA
 ACAGCGGGCCCCTGAGCAGCCCCGGAAGCAAGTGCCGCATTCTTCAGGAAGGAAGAGACCTGGGCA
 CCCAAGACCTGGTTTCTTCTTTCATTCTCCAGGAGACCCCTCCAGCTTTGTTTGAGATCCTGAA
 AATCTTGAAGAAGGTATTCCTCACCTTTCTTGCCCTTACCAGACACTGGAAGAGAATACTATAT
 TGCTCATTTAGCTAAGAAATAAATACATCTCATCTAACACACACGACAAAGAGAAGCTGTGCTTG
 CCCCAGGGGTGGGTATCTAGCTCTGAGATGAAGTCAAGTTATAGGAGAAAACCTCCATGCTGGACTC
 CATCTGGCATTCAAATCTCCACAGTAAATCCAAAGACCTCAAAAAAAAAAAAAAAAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 100

MKMQKGNVLLMFGLLLHLEAATNSNETSTSANTGSSVISSGASTATNSGSSVTSSGVSTATISGS
 SVTSNGVSIVTNSEFHTTSSGISTATNSEFSTASSGISIATNSESSTTSSGASTATNSESSTPSS
 GASTVTNSGSSVTSSGASTATNSESSTVSSRASTATNSESSTLSSGASTATNSDSSTTSSGASTA
 TNSESSTTSSGASTATNSESSTVSSRASTATNSESSTTSSGASTATNSESRTTNGAGTATNSES
 STTSSGASTATNSDSSTVSSGASTATNSESSTTSSGASTATNSESSTTSSGASTATNSDSSTTSS
 GAGTATNSESSTVSSGISTVTNSESSTPSSGANTATNSESSTTSSGANTATNSESSTVSSGASTA
 TNSESSTTSSGVSTATNSESSTTSSGASTATNSDSSTTSSSEASTATNSESSTVSSGISTVTNSES
 STTSSGANTATNSGSSVTSAGSGTAALTGMHTTSHSASTAVSEAKPGGSLVPWEIFLITLVSVVA
 AVGLFAGLFFCVRNSLSLRNTFNTAVYHPHGLNHGLGPGPGGNHGAPHRPRWSPNWFWRPVSII
 AMEMSGRNSGP

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 510-532

[illegible]

Important features of the protein:

amino acids 1-22

amino acids 44-63, 90-108, 354-377

FIGURE 103

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCTCCACGGCTCCTGCGCCTGAGACAGCTGGCCTGACC
TCCAAATCATCCATCCACCCCTGCTGTCATCTGTTTTTCATAGTGTGAGATCAACCCACAGGAATA
TCCATGGCTTTTGTGCTCATTTTGGTTCTCAGTTTCTACGAGCTGGTGTGAGGACAGTGGCAAGT
CACTGGACCGGGCAAGTTTGTCCAGGCCCTTGGTGGGGGAGGACGCCGTGTTCTCCTGCTCCCTCT
TTCCTGAGACCAAGTGCAGAGGCTATGGAAGTGCGGTTCTTCAGGAATCAGTTCCATGCTGTGGTC
CACCTCTACAGAGATGGGGAAGACTGGGAATCTAAGCAGATGCCACAGTATCGAGGGGAGAACTGA
GTTTGTGAAGGACTCCATTGCAGGGGGGCGTGTCTCTCTAAGGCTAAAAAACATCACTCCCTCGG
ACATCGGCCTGTATGGGTGCTGGTTTCAGTTCCAGATTTACGATGAGGAGGCCACCTGGGAGCTG
CGGGTGGCAGCACTGGGCTCACTTCCTCTCATTTCATCGTGGGATATGTTGACGGAGGTATCCA
GTTACTCTGCCTGTCTCAGGCTGGTTCCCCCAGCCCCACAGCCAAGTGGAAAGGTCCACAAGGAC
AGGATTTGTCTTCAGACTCCAGAGCAAATGCAGATGGGTACAGCCTGTATGATGTGGAGATCTCC
ATTATAGTCCAGGAAAATGCTGGGAGCATATTGTGTCCATCCACCTTGCTGAGCAGAGTCATGA
GGTGGAAATCCAAGGTATTGATAGGAGAGACGTTTTTCCAGCCCTACCTTGCGCCTGGCTCTTA
TTTTACTCGGGTTACTCTGTGGTGCCCTGTGTGGTGTGTGTCATGGGGATGATAATTGTTTTCTTC
AAATCCAAAGGGAAAATCCAGGCGGAAGTGGACTGGAGAAGAAAGCACGGACAGGCAGAAATGAG
AGACGCCCCGAAACACGCAGTGGAGGTGACTCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCG
TTTCTGATCTGAAAAGTGAACCATAGAAAAGTCCCCAGGAGGTGCCTCACTCTGAGAAGAGA
TTTACAAGGAAGAGTGTGGTGGCTTCTCAGGGTTTCCAAGCAGGGAGACATTACTGGGAGGTGGA
CGTGGGACAAAATGTAGGGTGGTATGTGGGAGTGTGTCGGGATGACGTAGACAGGGGGAAGAACA
ATGTGACTTTGTCTCCCAACAATGGGTATTGGGTCTCAGACTGACAACAGAACATTTGTATTTT
ACATTCAATCCCCATTTTATCAGCCTCCCCCCCAGCACCCTCTTACACGAGTAGGGGTCTTCCT
GGACTATGAGGGTGGGACCATCTCCTTCTTCAATACAAATGACCAGTCCCTTATTTATACCCTGC
TGACATGTGAGTTTGAAGGCTTGTGAGACCCTATATCCAGCATGCGATGTATGACGAGGAAAAG
GGGACTCCCATATTTCATATGTCCAGTGTCTGGGGATGAGACAGAGAAGACCCTGCTTAAAGGGC
CCCACACCACAGACCAGACACAGCCAAGGGAGAGTGTCTCCGACAGGTGGCCCCAGCTTCCTCT
CCGGAGCCTGCGCACAGAGAGTCAAGCCCCCACTCTCCTTTAGGGAGCTGAGGTTCTTCTGCCC
TGAGCCCTGCAGCAGCGGCAGTCAAGCTTCCAGATGAGGGGGGATTGGCCTGACCCTGTGGGAG
TCAGAAGCCATGGCTGCCCTGAAGTGGGGACGGAATAGACTCACATTAGGTTTAGTTTGTGAAAA
CTCCATCCAGCTAAGCGATCTTGAACAAGTCAACCTCCCAGGCTCCTCATTGTGTAGTCACGG
ACAGTGATTCTGCTTCCAGGTGAAGATTAAAGAGACAACGAATGTGAATCATGCTTGCAGGTT
TGAGGGCACAGTGTGCTAATGATGTGTTTTATATTATACATTTTCCACCATAAACTCTGTT
TGCTTATTCACATTAATTTACTTTTCTCTATACCAATCACCCATGGAATAGTTATTGAACACC
TGCTTTGTGAGGCTCAAAGAATAAAGAGGAGGTAGGATTTTCACTGATTCTATAAGCCCAGCAT
TACCTGATACCAAACAGGCAAGAAAACAGAAGAAGAGGAAGGAAAACACAGGTCCATATCC
CTCATTAAACACAGACACAAAAATTTCTAAATAAAATTTTAAACAAATTAACTAAACAATATATTA
AAGATGATATATACTACTCAGTGTGGTTTGTCCCAAAATGCAGAGTTGGTTTAAATTTAAAT
ATCAACCAGTGTAATTCAGCACATTAATAAAGTAAAAAGAAAACCATAAAAA

FIGURE 105

CCTTCACAGGACTCTTCATTGCTGGTTGGCAATGATGTATCGGCCAGATGTGGTGAGGGCTAGGAAAAGAG
TTTGTGGGAACCTGGGTTATCGGCCCTCGTCATCTTCATATCCCTGATGTCTGGCAGTGTGCATTGGA
CTCACTGTTTATTATGTGAGATATAATCAAAGAAGACCTACAATTACTATAGCACATTGTCATTTACAAC
TGACAAACTATATGCTGAGTTTGGCAGAGAGGCTTCTAACAATTTTACAGAAATGAGCCAGAGACTTGAAT
CAATGGTGAAAAATGCATTTTATAAATCTCCATTAAGGGAAGAATTTGTCAAGTCTCAGGTTATCAAGTTC
AGTCAACAGAAGCATGGAGTGTGGCTCATATGCTGTTGATTTGTAGATTTCACCTACTGAGGATCCTGA
AACTGTAGATAAAATTGTTCAACTTGTTTTACATGAAAAGCTGCAAGATGCTGTAGGACCCCTAAAGTAG
ATCCTCACTCAGTTAAATTAATAAATCAACAAGACAGAAACAGACAGCTATCTAAACCATTGCTGCGGA
ACACGAAGAAGTAAACTCTAGGTCAGAGTCTCAGGATCGTTGGTGGGACAGAAGTAGAAGAGGGTGAATG
GCCCCTGGCAGGCTAGCCTGCAGTGGGATGGGAGTCATCGCTGTGGAGCAACCTTAATTAATGCCACATGGC
TTGTGAGTGTCTCACTGTTTACAACATATAAGAACCCTGCCAGATGGACTGCTTCCTTTGGAGTAACA
ATAAACCTTCGAAATGAAACGGGGTCTCCGGAGAATAATTGTCCATGAAAAATACAAACACCCATCACA
TGACTATGATATTTCTCTGTCAGAGCTTTCTAGCCCTGTTCCCTACACAAATGCAGTACATAGAGTTTGTCT
TCCCTGATGCATCCTATGAGTTTCAACCAGGTGATGTGATGTTTGTGACAGGATTGGAGCACTGAAAAAT
GATGGTTACAGTCAAAATCATCTTCGACAAGCACAGGTGACTCTCATAGACGCTACAACTTGCAATGAACC
TCAAGCTTACAATGACGCCATAACTCCTAGAATGTTATGTGCTGGCTCCTTAGAAGGAAAAACAGATGCAT
GCCAGGTGACTCTGGAGGACCACTGGTTAGTTTACAGATGCTAGAGATATCTGGTACCTTGCTGGAATAGTG
AGCTGGGGAGATGAATGTGCGAAACCAACAAGCCTGGTGTATATACTAGAGTTACGGCCTTGCGGGACTG
GATTACTTCAAAAACCTGGTATCTTAAGAGACAAAAGCCTCATGGAACAGATAACATTTTTTTTTGTTTTTTG
GGTGTGGAGGCCATTTTATAGATACAGAATTGGAGAAGACTTGCAAAACAGCTAGATTGACTGATCTCA
ATAAACTGTTTGTCTGATGCATGTATTTCTTCCCAGCTCTGTTCCGCACGTAAGCATCCTGCTTCTGCCA
GATCAACTCTGTCTCTGTGAGCAATAGTTGAAACTTTATGTACATAGAGAAATAGATAATACAATATTAC
ATTACAGCCTGTATTCATTTGTTCTCTAGAAGTTTGTGCAAAATTTGACTTGTGACATAAATTTGTAAT
GCATATATACAATTTGAAGCACTCCTTTTCTTCAGTTCCTCAGCTCCTCTCATTTTCAGCAATATCCATTT
TCAAGGTGCAGAACAGGAGTGAAAGAAAATATAAGAAGAAAAAATCCCCCTACATTTTATTGGCACAGAA
AAGTATTAGGTGTTTTCTTAGTGGAATATTAGAAATGATCATATTATTATGAAAGGTCAAGCAAAGACA
GCAGAATACCAATCACTTCATCTTTAGGAAGTATGGGAACCTAAGTTAAGGAAGTCCAGAAAGAAGCCAAG
ATATATCCTTATTTTCAATTTCCAAACACTACTATGATAAATGTGAAGAAGATTCTGTTTTTTGTGACCT
ATAATAATTATACAACTTCATGCAATGTACTTGTCTAAGCAAATTAAGCAAATATTTATTTAACATTG
TTACTGAGGATGTCAACATATAACAATAAAATATAAATCACCCA

FIGURE 106

MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTNYNSTLSFTTDKLY
 AEFGREASNNFTEMSQRLESMVKNAFYKSPLREEFVKSQVIKFSQQKHGVLAHMLLICRFHSTED
 PETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTLGQSLRIVGG
 TEVEEGEWPWQASLQWDGSHRCGATLINATWLVSAAHCFTTYKNPARWTASFGVTIKPSKMKRGL
 RRIIVHEKYKHPSHDYDISLAELSSPVPTNAVHRVCLPDASYEFQPGDVMFVTGFGALKNDGYS
 QNHLRQAQVTLIDATTCNEPQAYNDAITPRMLCAGSLEGKTDACQGDGGPLVSSDARDIWIYLAG
 IVSWGDECAKPNKPGVYTRVTALRDWITSKTGI

Transmembrane domain:

amino acids 21-40 (type II)

FIGURE 108

MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMDYLNNVLTTLTAETRVEEAVILTYFPVVHP
 VMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMVPVQWSDMVT
 LKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTMDWPPDSCCVREFPGCSKQAHQ
 EDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMILTITLLWALYYDRREPGTDQM
 MSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL

Signal peptide:

amino acids 1-33

Transmembrane domains:

amino acids 12-35, 57-86, 94-114, 226-248

FIGURE 110

MPPFLLLTCLFITGTSVSPVALDPCSAYISLNEPWRNTDHLDESQGPPLCDNHVNGEWYHFTGMAGDAMP
 TFCIPENHCGTHAPVWLNGSHPLEGDGIVQRQACASFNGNCCLWNTTVEVKACPGGYVYRLTKPSVCFHV
 YCGHFYDIDCEDCHGSCSDTSECTCAPGTVLGPDRQTCFDENECEQNNGGCSEICVNLKNSYRCECGVGRV
 LRS DGKTCEDVEGCHNNNGGCSHSLGSEKGYQCECPRGLVLS EDNHTCQVPVLCKSNAIEVNI PRELVGG
 LELFLTNTSCRGVSN GTHVNILFSLKTCGTVVDVNDKIVASNLVTGLPKQTPGSSGDFIIRTSKLLIPVT
 CEFPRLYTISEGYVPNLRNSPLEIMSRNHGIFPFTLEIFKDNEFE EPYREALPTLKL RDSLYFGIEPVVHV
 SGL ESLVESC FATPTSKIDEVLKYLLIRDGCVSDDSVKQYTSRDHLAKHFQVPVFKFVGKDHKEVFLHCRV
 LVCGVLDESRCAQGCCHRRMRRGAGGEDSAGLQGQTTLTGGP IRIDWED

Important features of the protein:

Signal peptide:

amino acids 1-16

N-glycosylation sites.

amino acids 89-93, 116-120, 259-263, 291-295, 299-303

Tyrosine kinase phosphorylation sites.

amino acids 411-418, 443-451

N-myristoylation sites.

amino acids 226-232, 233-239, 240-246, 252-258, 296-302, 300-306,
 522-528, 531-537

Aspartic acid and asparagine hydroxylation site.

amino acids 197-209

ZP domain proteins.

amino acids 431-457

Calcium-binding EGF-like proteins.

amino acids 191-212, 232-253

FIGURE 111

GAGAGAGGCAGCAGCTTGCTCAGCGGACAAGGATGCTGGGCGTGAGGGACCAAGGCCTGCCCTGCACTCGG
 GCCTCCTCCAGCCAGTGCTGACCAGGGACTTCTGACCTGCTGGCCAGCCAGGACCTGTGTGGGGAGGCCCT
 CCTGCTGCCTTGGGGTGACAATCTCAGCTCCAGGCTACAGGGAGACCGGGAGGATCACAGAGCCAGCATGT
 TACAGGATCCTGACAGTGATCAACCTCTGAACAGCCTCGATGTCAAACCCCTGCGCAAACCCCGTATCCCC
 ATGGAGACCTTCAGAAAGGTGGGGATCCCCATCATCATAGCACTACTGAGCCTGGCGAGTATCATCATTGT
 GGTGTCTCATCAAGGTGATCTGGATAAATACTACTTCTCTGCGGGCAGCCTCTCCACTTCATCCGGA
 GGAAGCAGCTGTGTGACGGAGAGCTGGACTGTCCCTTGGGGGAGGACGAGGAGCACTGTGTCAAGAGCTTC
 CCCGAAGGGCCTGCAGTGGCAGTCCGCCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGGACTCGGCCAC
 AGGGAAGTGGTTCTCTGCCTGTTTCGACAACCTTCACAGAAGCTCTCGCTGAGACAGCCTGTAGGCAGATGG
 GCTACAGCAGAGCTGTGGAGATTGGCCCAGACCAGGATCTGGATGTTGTTGAAATCACAGAAAACAGCCAG
 GAGCTTCGCATGCGGAACCTCAAGTGGGCCCTGTCTCTCAGGCTCCCTGGTCTCCCTGCACTGTCTTGCTG
 TGGGAAGAGCCTGAAGACCCCCCGTGTGGTGGGTGGGGAGGAGGCTCTGTGGATTCTTGGCCTTGGCAGG
 TCAGCATCCAGTACGACAAACAGCACGTCTGTGGAGGGAGCATCCTGGACCCCCACTGGGTCTCACGGCA
 GCCCACTGCTTCAGGAAACATACCGATGTGTCAACTGGAAGGTGCGGGCAGGCTCAGACAAATGGGCAG
 CTTCCTCCATCCCTGGCTGTGGCCAAGATCATCATATTGAATTCAACCCCATGTACCCCAAAGACAATGACA
 TCGCCCTCATGAAGCTGCAGTTCCTCACTCTTCTCAGGCACAGTCAGGCCCATCTGTCTGCCCTTCTTT
 GATGAGGAGCTCACTCCAGCCACCCCACTCTGGATCATTGGATGGGGCTTTACGAAGCAGAATGGAGGGAA
 GATGTCTGACATACTGCTGCAGGCGTCAGTCCAGGTCATTGACAGCACCGGTGCAATGCAGACGATGCGT
 ACCAGGGGGAAGTCACCGAGAAGATGATGTGTGCAGGCATCCCGGAAGGGGTGTGGACACCTGCCAGGGT
 GACAGTGGTGGGCCCTGATGTACCAATCTGACCAGTGGCATGTGGTGGGCATCGTTAGCTGGGGCTATGG
 CTGCGGGGGCCCGAGCACCCAGGAGTATACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATGTCT
 GGAAGGCTGAGCTGTAATGCTGCTGCCCCCTTTCAGTGTCTGGGAGCCGCTTCCTTCCTGCCCTGCCACCT
 GGGGATCCCCCAAAGTCAGACACAGAGCAAGAGTCCCCTTGGGTACACCCCTCTGCCACAGCCTCAGCAT
 TTCTTGAGCAGCAAAGGGCCTCAATTCCTGTAAGAGACCCTCGCAGCCCAGAGCGCCCAGAGGAAGTCA
 GCAGCCCTAGCTCGGCCACACTTGGTGCTCCAGCATCCAGGGAGAGACACAGCCACTGAACAAGGTCT
 CAGGGGTATTGCTAAGCCAAGAAGGAACCTTCCACACTACTGAATGGAAGCAGGCTGTCTTGTAAAAGCC
 CAGATCACTGTGGCTGGAGAGGAGAAGGAAAGGTCTGCGCCAGCCCTGTCCGTCTTACCCATCCCCAA
 GCCTACTAGAGCAAGAAACAGTTGTAATATAAAATGCACTGCCCTACTGTTGGTATGACTACCGTTACCT
 ACTGTTGTATTGTTATTACAGCTATGGCCACTATTATTAAAGAGCTGTGTAACATCTCTGGCAAAAAAAA
 AAAA

$$\frac{d}{dt} \left(\frac{\partial L}{\partial \dot{x}} \right) = \frac{\partial L}{\partial x}$$

Transmembrane domain:
amino acids 32-53 (typeII)

FIGURE 113

GGCTGGACTGGAACCTCTGGTCCCAAGTGATCCACCCGCCTCAGCCTCCCAAGGTGCTGTGATTA
TAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACCTTTTCAGCAACTAAAAAGCCACAGGAGT
TGAAGTGTAGGATTCTGACTATGCTGTGGTGGCTAGTGCTCCTACTCCTACCTACATTAAATC
TGTTTTTTGTCTCTTGTAAGTACGCTTTACCTTCCTAACACAGAGGATCTGTCACTGTGGCTCT
GGCCCAAACCTGACCTTCACTCTGGAACGAGAACAGAGGTTTCTACCCACACCGTCCCCTCGAAG
CCGGGGACAGCCTCACCTTGCTGGCCTCTCGCTGGAGCAGTGCCCTACCAACTGTCTCACGTCT
GGAGGCACTGACTCGGGCAGTGAGGTAGCTGAGCCTCTGGTAGCTGCGGCTTCAAGGTGGGC
CTTGCCCTGGCCGTAGAAGGGATTGACAAGCCCGAAGATTTATAGGCGATGGCTCCCACTGCC
AGGCATCAGCCTTGCTGTAGTCAATCACTGCCCTGGGGCCAGGACGGGCCGTGGACACCTGCTCA
GAAGCAGTGGGTGAGACATCACGCTGCCCGCCATCTAACCTTTTCATGTCTGCACATCACCTG
ATCCATGGGCTAATCTGAAGTCTGTCCCAAGGAACCCAGAGCTTGAGTGAGCTGTGGCTCAGACC
CAGAAGGGGTCTGCTTAGACCACCTGGTTTATGTGACAGGACTTGCAATCTCTCTGGAACATGAGG
GAACGCCGGAGGAAGCAAAGTGGCAGGGAAGGAACCTGTGCCAAATATGGGTGAGAAAAGATG
GAGGTGTGGGTATCACAAAGGCATCGAGTCTCTGCATTCACTGGACATGTGGGGGAAGGGCTG
CCGATGGCGCATGACACACTCGGGACTCACCTCTGGGGCCATCAGACAGCCGTTTCCGCCCGAT
CCACGTACCAGCTGCTGAAGGGCAACTGCAGGCCGATGCTCTCATCAGCCAGGCAGCAGCCAAAA
TCTGCGATCACCAGCCAGGGGCAGCCGCTCTGGGAAGGAGCAAGCAAAGTGACCATTTCTCCTCCC
CTCCTTCCCTCTGAGAGGCCCTCCTATGTCCCTACTAAAGCCACCAGCAAGACATAGCTGACAGG
GGCTAATGGCTCAGTGTGGGCCAGGAGGTGAGCAAGGCCTGAGAGCTGATCAGAAGGGCCTGCT
GTGCGAACACGGAAATGCCTCCAGTAAGCACAGGCTGCAAAATCCCAGGCAAAGGACTGTGTGG
CTCAATTTAAATCATGTTCTAGTAATTGGAGCTGTCCCAAGACCAAAGGAGCTAGAGCTTGGTT
CAAATGATCTCCAAGGGCCCTTATACCCAGGAGACTTTGATTGAAATTTGAAACCCCAAATCCA
AACCTAAGAACCAGGTGCATTAAGAATCAGTTATTGCCGGGTGTGGTGGCCTGTAATGCCAACAT
TTTGGGAGGCCGAGGCGGTAGATCACCTGAGGTGAGGAGTTCAAGACCAGCCTGGCCAACATGG
TGAAACCCCTGTCTCTACTAAAAATACAAAAAACTAGCCAGGCATGGTGGTGTGTGCCTGTATC
CCAGCTACTCGGGAGGCTGAGACAGGAGAATTACTTGAACCTGGGAGGTGAAGGAGGCTGAGACA
GGAGAATCACTTCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGAAAAATAAAAAAGAATTA
TGGTTATTTGTAA

FIGURE 114

MLWWLVLLLLPTLKSVFCSLVTSLYLPNTEDLSLWLWPKPDLHSGTRTEVSTHTVPSKPGTASPC
WPLAGAVPSPTVSRLEALTRAVQVAEPLGSCGFQGGPCPGRRRD

Signal peptide:
amino acids 1-15

FIGURE 117

GAGCTCCCCCTCAGGAGCGCGTTAGCTTCACACCTTCGGCAGCAGGAGGGCGGCAGCTTCTCGCAGGCGGCA
GGGCGGGCGGCCAGGATC**ATG**TCCACCACCACATGCCAAGTGGTGGCGTTCCCTCTGTCCATCCTGGGGCT
GGCCGGCTGCATCGCGGCCACCGGGATGGACATGTGGAGCACCAGGACCTGTACGACAACCCGTCACCT
CCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTGCGTGAGGCAGAGTTCAGGCTTCACCGAATGCAGGCCC
TATTTACCATCCTGGGACTTCCAGCCATGCTGCAGGCAGTGCGAGCCCTGATGATCGTAGGCATCGTCTT
GGGTGCCATTGGCCTCCTGGTATCCATCTTTGCCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTG
CCAAAGCCAACATGACACTGACCTCCGGGATCATGTTTATTGTCTCAGGTCTTTGTGCAATTGCTGGAGTG
TCTGTGTTTGCCAACATGCTGGTGACTAACTTCTGGATGTCCACAGCTAACATGTACACCGGCATGGGTGG
GATGGTGCAGACTGTTTACAGCCAGGTACACATTGGTGCGGCTCTGTTCTGGGCTGGGTGCGCTGGAGGCC
TCACACTAATTGGGGGTGTGATGATGTGCATCGCCTGCCGGGGCCTGGCACCAGAAAGAAACCACTACAAA
GCCGTTTCTTATCATGCCCTCAGGCCACAGTGTGCTTACAAGCCTGGAGGCTTCAAGGCCAGCACTGGCTT
TGGGTCCAACACCAAAAACAAGAAGATATACGATGGAGGTGCCCGCACAGAGGACGAGGTACAATCTTATC
CTTCCAAGCAGCACTATGTG**TAA**TGCTCTAAGACCTCTCAGCACGGGCGGAAGAACTCCCGGAGAGCTCA
CCCAAAAACAAGGAGATCCCATCTAGATTCTTCTTGCTTTTGAATCACAGCTGGAAGTTAGAAAAGCCT
CGATTTTCATCTTTGGAGAGGCCAAATGGTCTTAGCCTCAGTCTCTGTCTCTAAATATTCACCATAAAAACA
GCTGAGTTATTTATGAATTAGAGGCTATAGCTCACATTTTCAATCCTCTATTTCTTTTTTAAATATAACT
TTCTACTCTGATGAGAGAATGTGGTTTAAATCTCTCTCACATTTTGATGATTTAGACAGACTCCCCCTC
TTCTCTAGTCAATAAACCATTGATGATCTATTTCCAGCTTATCCCAAGAAAACCTTTTGAAAGGAAA
GAGTAGACCCAAAGATGTTATTTCTGCTGTTGAATTTGTCTCCCCACCCCAACTTGGCTAGTAATAA
ACACTTACTGAAGAAGAAGCAATAAGAGAAGATATTTGTAATCTCTCCAGCCCATGATCTCGGTTTTCTT
ACACTGTGATCTTAAAGTTACCAAACCAAGTCATTTTCAGTTTGAGGCAACCAACCTTTCTACTGCTG
TTGACATCTTCTTATTACAGCAACACCATTCTAGGACTTTCTGAGCTCTCCACTGGAGTCCCTCTTCTGT
CGCGGGTCAGAAATTGTCCCTAGATGAATGAGAAAATTATTTTTTTAATTTAAGTCCTAAATATAGTTAA
AATAAATAATGTTTTAGTAAATGATACACTATCTCTGTGAAATAGCCTCACCCCTACATGTGGATAGAAG
GAAATGAAAAATAATGCTTTGACATTGTCTATATGGTACTTTGTAAAGTCATGCTTAAGTACAAATTC
ATGAAAAGCTCACACCTGTAATCCTAGCACTTTGGGAGGCTGAGGAGGAAGGATCACTTGAGCCCAGAAGT
TCGAGACTAGCCTGGGCAACATGGAGAAGCCCTGTCTCTACAAAATACAGAGAGAAAAATCAGCCAGTCA
TGGTGGCATACACCTGTAGTCCCAGCATTCGGGAGGCTGAGGTGGGAGGATCACTTGAGCCCAGGGAGGT
TGGGGCTGCAGTGAGCCATGATCACACCACTGCACTCCAGCCAGGTGACATAGCGAGATCCTGTCTAAAAA
AATAAAAAATAAATAATGGAACACAGCAAGTCCTAGGAAGTAGGTTAAACTAATTCCTTTAA

FIGURE 118

MSTTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLRSCVRQSSGFTECRP
YFTILGLPAMLQAVRALMIVGIVLGAIGLLVSI FALKCIRIGSMEDSAKANMTLTSGIMFIVSGL
CAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWVAGGLTLIGGVMMCIA
CRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKIYDGGARTEDEVQSYPSKHDY
V

Signal peptide:

amino acids 1-23

Transmembrane domains:

amino acids 81-100, 121-141, 173-194

FIGURE 119

GGAAAACTGTTCTTCTGTGGCACAGAGAACCCTGCTTCAAAGCAGAAGTAGCAGTTCCGGAGTCC
 AGCTGGCTAAAACTCATCCCAGAGGATAATGGCAACCCATGCCTTAGAAATCGCTGGGCTGTTTCTTG
 GTGGTGTGGAATGGTGGGCACAGTGGCTGTCACTGTGCCTCAGTGGAGAGTGTGGCCTTCATT
 GAAAACAACATCGTGGTTTTTGAAGCTTCTGGGAAGGACTGTGGATGAATTGCGTGAGGCAGGCTAA
 CATCAGGATGCAGTGCAAAATCTATGATTCCCTGTGGCTCTTCTCCGGACCTACAGGCAGCCAGAG
 GACTGATGTGTGCTTCCGTGATGTCCTTCTTGGCTTTCATGATGGCCATCCTTGGCATGAAATGC
 ACCAGGTGCACGGGGGACAATGAGAAGGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTTCAT
 CATCACGGGCATGGTGGTGTCTATCCCTGTGAGCTGGGTTGCCAATGCCATCATCAGAGATTTCTATA
 ACTCAATAGTGAATGTTGCCCAAAACGTGAGCTTGAGAAGCTCTCTACTTAGGATGGACCACGGCA
 CTGGTGTGATTGTTGGAGGAGCTCTGTTCTGCTGCGTTTTTGTGCAACGAAAAGAGCAGTAGCTA
 CAGATACTCGATACCTTCCCATCGCACACCCAAAAAGTTATCACACCGAAAGAAGTCACCGAGCG
 TCTACTCCAGAAGTCAGTATGTAGTTGTGTATGTTTTTAACTTTACTATAAAGCCATGCAAATG
 ACAAAAATCTATATTACTTTCTCAAAATGGACCCCAAGAACTTTGATTACTGTTCTTAATGCGCT
 AATCTTAATTACAGGAAGTGTGCATCAGCTATTTATGATTCTATAAGCTATTTACAGAGAATGAGATA
 TTAAACCAATGCTTTGATTGTTCTAGAAAGTATAGTAATTTGTTTCTAAGGTGGTTCAAGCATCTA
 CTCTTTTATCATTTACTTCAAAATGACATTGCTAAAGACTGCATTATTTACTACTGTAATTTCTCC
 ACGACATAGCATTATGTACATAGATGAGTGTAAACATTTATATCTCACATAGAGACATGCTTATATGGT
 TTTATTTAAATGAAATGCCAGTCCATTACACTGAATAAATAGAACTCAACTATTGCTTTTCAGGGAA
 ATCATGGATAGGGTTGAAGAAGGTTACTATTAATTGTTTAAAAACAGCTTAGGGATTAATGTCTCCCA
 TTTATAATGAAGATTAAATGAAGGCTTTAATCAGCATTGTAAAGGAAATTGAATGGCTTTCTGATAT
 GCTGTTTTTTAGCCTAGGACTTAGAAATCCTAACTTCTTTATCCTCTTCTCCAGAGGCTTTTTTTTT
 CTTGTGTATTAAATTAACATTTTTTAAACGCAGATATTTGTCAAGGGGCTTTGCATTCAAACGCTT
 TTCCAGGGCTATACTCAGAAGAAAGATAAAAGTGTGATCTAAGAAAAAGTGATGGTTTTAGGAAAGTG
 AAAATATTTTGTGTTTTGATTTGAAGAAGATGATGCATTTTGACAAGAAATCATATATGTATGGAT
 ATATTTTAATAAGTATTTGAGTACAGACTTTGAGGTTTCATCAATATAAATAAAGAGCAGAAAAATA
 TGTCTTGGTTTTTCATTTGCTTACCAAAAAACACAACAAAAAAGTTGTCCTTTGAGAACTTCACCT
 GCTCCTATGTGGGTACCTGAGTCAAAATGTGCATTTTTGTTCTGTGAAAAATAAATTTCTTCTTGTA
 CCATTTCTGTTTAGTTTTACTAAAATCTGTAAATACTGTATTTTTCTGTTTATCCAAATTTGATGAA
 ACTGACAATCCAATTTGAAAGTTGTGTGACGCTCTGTCTAGCTTAAATGAATGTGTTCTATTTGCTT
 TATACATTTATATTAATAAATTGTACATTTTCTAATT

FIGURE 120

MATHALEIAGLFLGGVGMVGTVAVTVMPPQWRVSAFIENNIVVFENFW EGLWMNCVRQANIRMQCK
IYDSL LALSPDLQAARGLMCAASVMSFLAFMAILGMKCTRCTGDNEKVKAHILLTAGIIFIITG
MVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVFCCNEKSSSY
RYSIPSHRTTQKSYHTGKKSPSVYSRSQYV

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 82-101, 118-145, 164-188

$$E = \frac{1}{\epsilon_0} \left(\frac{q}{r^2} + \frac{q}{r^2} + \frac{q}{r^2} + \dots \right) = \frac{1}{\epsilon_0} \left(\frac{q}{r^2} + \frac{q}{r^2} + \frac{q}{r^2} + \dots \right)$$

FIGURE 122

MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAQVPGR
DGSPGANVIPGTPGIPGRDGFKEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIAECTFTK
MRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECGGLPIEAIYLDQGSPEMNSTINIHRIS
SVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIEELPK

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217

FIGURE 123

GCTGAGCGTGTGCGCGGTACGGGGCTCTCCTGCCTTCTGGGCTCCAACGCAGCTCTGTGGCTGAA
CTGGGTGCTCATCACGGGAAGTGTGGGCTATGGAATACAGATGTGGCAGCTCAGGTAGCCCCAA
ATTGCCTGGAAGAATACATCATGTTTTTCGATAAGAAGAAATTGTAGGATCCAGTTTTTTTTTTA
ACCGCCCCCTCCCCACCCCCCAAAAACTGTAAAGATGCAAAAACGTAATATCCATGAAGATCC
TATTACCTAGGAAGATTTTGATGTTTTGCTGCGAATGCGGTGTTGGGATTTATTTGTTCTTGGAG
TGTTCTGCGTGGCTGGCAAAGAATAATGTTCCAAAATCGGTCCATCTCCCAAGGGGTCCAATTTT
TCTTCTGGGTGTCAGCGAGCCCTGACTCACTACAGTGCAGCTGACAGGGGCTGTCATGCAACTG
GCCCCAAGCCAAAGCAAAGACCTAAGGACGACCTTTGAACAATACAAAGGATGGGTTTCAATG
TAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTTATAGCCCCACTGTCTTACTGACAATG
CTTTCTTCTGCCGAACGAGGATGCCCTAAGGGCTGTAGGTGTGAAGGCAAAATGGTATATTGTGA
ATCTCAGAAATTACAGGAGATACCCCTCAAGTATATCTGCTGGTTGCTTAGGTTTGTCCCTTCGCT
ATAACAGCCTTCAAAAACTTAAGTATAATCAATTTAAAGGGCTCAACCAGCTCACCTGGCTATAC
CTTGACCATAACCATATCAGCAATATTGACGAAAATGCTTTAATGGAATACGCAGACTCAAAGA
GCTGATTCTTAGTTCCAAATAGAATCTCCTATTTTCTTAACAATACCTTCAGACCTGTGACAAAT
TACGGAACCTGGATCTGTCTTATAATCAGCTGCATTCTCTGGGATCTGAACAGTTTCGGGGCTTG
CGGAAGCTGTGAGTTTACATTTACGGTCTAATCCCTGAGAACCATCCCTGTGCGAATATTCCA
AGACTGCCGCAACCTGGAACCTTTGGACCTGGGATATAACCGGATCCGAAGTTTAGCCAGGAATG
TCTTTGCTGGCATGATCAGACTCAAAGAACTTCACCTGGAGCACAATCAATTTTCCAAGCTCAAC
CTGGCCCTTTTCCAAGGTTGGTCAGCCTTCAGAACCTTTACTTGCACTGGAATAAAATCAGTGT
CATAGGACAGACCATGTCTGACCTGGAGCTCCTTACAAAGGCTTGATTTATCAGGCAATGAGA
TCGAAGCTTTCAGTGGACCCAGTGTTCAGTGTGTCCGAATCTGCAGCGCTCAACCTGGAT
TCCAACAAGCTCACATTTATTGGTCAAGAGATTTTGGATTCTTGGATATCCCTCAATGACATCAG
TCTTGCTGGGAATATATGGGAATGCAGCAGAAATATTTGCTCCCTTGTAACCTGGCTGAAAAGTT
TTAAAGGTCTAAGGGAGAATACAATTATCTGTGCCAGTCCCAAAGAGCTGCAAGGAGTAAATGTG
ATCGATGCAGTGAAGAACTACAGCATCTGTGGCAAAAGTACTACAGAGAGGTTTGATCTGGCCAG
GGCTCTCCCAAGCCGACGTTTAAAGCCCAAGCTCCCAAGCCGAAGCATGAGAGCAAAACCCCTT
TGCCCCGACGGTGGGAGCCACAGAGCCCGGCCAGAGACCGATGCTGACGCCGAGCACATCTCT
TTCCATAAAATCATCGCGGGCAGCGTGGCGCTTTTCTGTCCGTGCTCGTCATCTGCTGTTAT
CTACGTGTCTGGAAGCGGTACCTTGCGAGCATGAAGCAGCTGCAGCAGCGCTCCCTCATGCGAA
GGCAGGAAAAAGAAAAGACAGTCCCTAAAGCAAATGACTCCAGCACCAGGAATTTATGTA
GATTATAAACCCACCAACAGGAGACCGAGATGCTGCTGAATGGGACGGGACCCCTGCACCTA
TAACAAATCGGGCTCCAGGGAGTGTGAGGTATGAACCATGTGATAAAAAGAGCTCTTAAAGCT
GGGAAATAAGTGGTGCTTTATTGAACTCTGGTGACTATCAAGGGAACCGGATGCCCCCCTCCCC
TTCCCTCTCCCTCTCACTTTGGTGGCAAGATCCTTCCTTGTCGTTTTAGTGCAATTCATAATCT
GGTCATTTTCTCTCATACATAATCAACCCATTGAAATTTAAATACCACAATCAATGTGAAGCTT
GAACTCCGGTTAATATAATACCTATTGTATAAGACCCCTTACTGATTCCATTAATGTGCGATTT
GTTTTAAGATAAACTTCTTTCATAGGTAAAAA

FIGURE 124

MGFNVIRLLSGSAVALVIAPTVLLTMLSSAERGCPKGCRCEGKMVYCESQKLQEIPSSISAGCLG
LSLRYNLSQKLKYNQFKGLNQLTWLYLDHNHISNIDENAFNGIRRLKELILSSNRISYFLNNTFR
PVTNLRNLDLSYNQLHSLGSEQFRGLRKLLSLHLRSNSLRTIPVRI FQDCRNLELLDLGYNRIRS
LARNVFAGMIRLKEHLEHNQFSKLNALFPRLVSLQNLQWNKISVIGQTMSTWSSQLRLDL
SGNEIEAFSGPSVFQCVPNLQRLNLDNKLTFIQEILDSWISLNDISLAGNIWECSRNICSLVN
WLKSFKGLRENTIICASPKELQGVNVIDAVKNYSICGKSTTERFDLARALPKPTFKPKLPRPKHE
SKPPLPPTVGATEPGPETDADAEHISFHKI IAGSVALFLSVLVILLVIYVSWKRYPASMKQLQQR
SLMRRHRKKKRQSLKQMTPTSTQEFYVDYKPTNTETSEMLLNGTGPCITYNKSGSRECEV

Important features of the protein:

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 420-442

N-glycosylation sites.

amino acids 126-129, 357-360, 496-499, 504-507

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 465-468

Tyrosine kinase phosphorylation site.

amino acids 136-142

N-myristoylation sites.

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

FIGURE 125

CCGTTATCGTCTTGCGCTACTGCTGAATGTCGGTCCCGGAGGAGGAGGAGAGGCTTTTGCCGCTG
 ACCCAGAGATGGCCCCGAGCGAGCAAATTCCTACTGTCCGGCTGCGCGGCTACCGTGCCCGAGCT
 AGCAACCTTTCCCTTGATCTCACAAAACTCGACTCCAAATGCAAGGAGAAGCAGCTCTTGCTC
 GGTGGGAGACGGTGCAAGAGAATCTGCCCCCTATAGGGGAATGGTGCGCACAGCCCTAGGGATC
 ATTGAAGAGGAAGGCTTTCTAAAGCTTTGGCAAGGAGTGACACCCGCCATTTACAGACACGTAGT
 GTATTCTGGAGGTCGAATGGTCAATATGAACATCTCCGAGAGGT'TGTGTTTGGCAAAAGTGAAG
 ATGAGCATTATCCCCTTTGGAAATCAGTCATTGGAGGGATGATGGCTGGTGTATTGGCCAGTTT
 TTAGCCAATCCAAC TGACCTAGTGAAGGTTGAGATGCAATGGAAGGAAAAGGAAACTGGAAGG
 AAAACCATTGCGATTTCGTGGGTGACATCATGCAATTTGCAAAAATCTTAGCTGAAGGAGGAATAC
 GAGGGCTTTGGGCAGGCTGGGTACCCAATATACAAAGAGCAGCAC TGGTGAATATGGGAGATTTA
 ACCACTTATGATACAGTGAAACACTACTTGGTATTGAATACACCATTGAGGACAATATCATGAC
 TCACGGTTTATCAAGTTTATGTTCTGGACTGGTAGCTTCTATTCTGGGAACACCAGCCGATGTCA
 TCAAAAGCAGAATAATGAATCAACCACGAGATAACAAGGAAGGGGACTTTTGTATAAATCATCG
 ACTGACTGCTTGATTGAGGCTGTTCAAGGTGAAGGATTCATGAGTCTATATAAAGGCTTTTACC
 ATCTTGGCTGAGAATGACCCCTTGGTCAATGGTGTCTGGCTTACTTATGAAAAAATCAGAGAGA
 TGAGTGGAGTCAGTCCATTTTAA

FIGURE 126

MSVPEEEERLLPLTQRWPRASKFLLSGCAATVAELATFPLDLTKTRLQMQGEAALARLGDGARES
APYRGMVRTALGIIEEGFLKLWQGVTPIYRHVVYSGGRMVTYEHLEVVFGKSEDEHYPLWKS
VIGGMMAGVIGQFLANPTDLVKVQMMEGKRKLEGKPLRFRGVHHAFAKILAEGGIRGLWAGWVP
NIQRAALVNMGDLTTYDTVKHYLVNTPLEDNIMTHGLSSLCSGLVASILGTPADVIKSRIMNP
RDKQGRGLLYKSSTDCLIQAVQGEFMSLYKGFLPSWLRMTPWSMVFWLTYEKIREMSGVSPF

Transmembrane domains:

amino acids 25-38, 130-147, 233-248

FIGURE 128

MARPGMERWRDRLALVTGASGGIGA AAVARALVQQGLKVVG CARTVGNIEELAAECKSAGYPGTLI
PYRCDLSNEEDILSMFSAIRSQHSGVDICINNAGLARPD TLLSGSTSGWKDMFNVNVLALSICTR
EAYQSMKERNVDDGHIININMSGHRVLP LSVTHFY SATKYAVTALTEGLRQELREAQTHIRATC
ISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVLSTPAHIQIGDIQMRPTEQVT

Important features of the protein:

Signal peptide:

amino acids 1-17

N-myristoylation sites.

amino acids 18-24, 21-27, 22-28, 24-30, 40-46, 90-96, 109-115,
199-205

Short-chain alcohol dehydrogenase.

amino acids 30-42, 104-114

FIGURE 129

AACTTCTACATGGGGCTCCTGCTGCTGGTGCCTTCCTCAGCCTCCTGCCGGTGGCCTACACCAT
CATGTCCCTCCCACCTCCTTTGACTGCGGGCCGTTTCAGGTGCAGAGTCTCAGTTGCCCGGGAGC
ACCTCCCCTCCCGAGGCAGTCTGCTCAGAGGGCCTCGGCCAGAATTCCAGTTCTGGTTTCATGC
CAGCCTGTAAAAGGCCATGGAACCTTTGGGTGAATCACCGATGCCATTTAAGAGGGTTTTCTGCCA
GGATGGAAATGTTAGGTCGTTCTGTGTCTGCGCTGTTTCATTTAGTAGCCACCAGCCACCTGTGG
CCGTTGAGTGCTTGAAATTGAGGAACTGAGAAAATTAATTTCTCATGTATTTTCTCATTATTTA
TTAATTTTTAACTGATAGTTGTACATATTTGGGGGTACATGTGATATTTGGATACATGTATACAA
TATATAATGATCAAATCAGGGTAACTGGGATATCCATCACATCAAACATTTATTTTTATTCTTT
TTAGACAGAGTCTCACTCTGTCACCCAGGCTGGAGTGCAGTGGTGCCATCTCAGCTTACTGCAAC
CTCTGCCTGCCAGGTTCAAGCGATTCTCATGCCTCCACCTCCCAAGTAGCTGGGACTACAGGCAT
GCACCACAATGCCCAACTAATTTTTGTATTTTAGTAGAGACGGGGTTTTGCCATGTTGCCCAGG
CTGGCCTTGAACTCCTGGCCTCAAACAATCCACTTGCCCTCGGCCTCCCAAAGTGTTATGATTACA
GGCGTGAGCCACCGTGCCTGGCCTAAACATTTATCTTTCTTTGTGTTGGGAACTTTGAAATTAT
ACAATGAATTATTGTTAACTGTCATCTCCCTGCTGTGCTATGGAACACTGGGACTTCTTCCCTCT
ATCTAACTGTATATTTGTACCAGTTAACCAACCGTACTTCATCCCCACTCCTCTCTATCCTTCCC
AACCTCTGATCACCTCATTCTACTCTCTACCTCCATGAGATCCACTTTTTAGCTCCCACATGTG
AGTAAGAAAATGCAATATTTGTCTTTCTGTGCTGGCTTATTTCACTTAACATAATGACTTCCTG
TTCCATCCATGTTGCTGCAAATGACAGGATTTCGTTCTTAATTTCAATTAATAAACCACACATG
GCAAAAA

FIGURE 130

MGLLLLVLFLSLLPVAYTIMSLPPSFDCGPFRCRVSVAREHLPSRGSLLRGPRPRIPVLVSCQPV
KGGHTLGESEMPFKRVFCQDGNVRSFCVCAVHFSSHQPPVAVECLK

Important features of the protein:

Signal peptide:

amino acids 1-18

N-myristoylation site.

amino acids 86-92

Zinc carboxypeptidases, zinc-binding region 2 signature.

amino acids 68-79

FIGURE 131

TTCTGAAGTAACGGAAGCTACCTTGTATAAAGACCTCAACACTGCTGACCATGATCAGCGCAGCCTGGAGC
ATCTTCTCATCGGGACTAAAATTGGGCTGTTCCTTCAAGTAGCACCTCTATCAGTTATGGCTAAATCCTG
TCCATCTGTGTGCTGCGTGCATGCGGGTTTCATTACTGTAATGATCGCTTTCTGACATCCATTCCAACAG
GAATACCAGAGGATGCTACAACTCTCTACCTTCAGAACAACCAATAAATAATGCTGGGATTCCTTCAGAT
TTGAAAACTTGCTGAAAGTAGAAAGAATATACCTATACCACAACAGTTTAGATGAATTTCCCTACCAACCT
CCCAAAGTATGTAAAAGAGTTACATTTGCAAGAAAATAACATAAGGACTATCACTTATGATTACATTCAA
AAATCCCTATCTGGAAGAATTACATTTAGATGACAACCTCTGTCTCTGCAGTTAGCATAGAAGAGGGAGCA
TTCCGAGACAGCAACTATCTCCGACTGCTTTTCTGTCCCGTAATCACCTTAGCACAAATCCCTGGGGTTT
GCCCAGGACTATAGAAGAACTACGCTTGGATGATAATCGCATATCCACTATTTTCATCACCATCTCTCAAG
GTCTCACTAGTCTAAAACGCCTGGTTCTAGATGGAACTGTGGAACAATCATGGTTTAGGTGACAAAGTT
TTCTTCAACCTAGTTAATTTGACAGAGCTGTCCCTGGTGCAGGAAATCCCTGACTGCTGCACCAAGTAAACCT
TCCAGGCACAAACCTGAGGAAGCTTTATCTTCAAGATAACCACATCAATCGGGTGCCCCCAATGCTTTTT
CTTATCTAAGGCAGCTCTATCGACTGGATATGTCCAATAATAACCTAAGTAATTTACCTCAGGGTATCTTT
GATGATTTGGACAATATAACACAACCTGATTCTTCGCAACAATCCCTGGTATTGCGGGTGCAAGATGAAATG
GGTACGTGACTGGTTACAATCACTACCTGTGAAGGTCAACGTGCGTGGGCTCATGTGCCAAGCCCCAGAAA
AGGTTCTGTTGGGATGGCTATTAAGGATCTCAATGCAGAACTGTTTGATTGTAAGGACAGTGGGATTGTAAGC
ACCATTGAGATAACCACTGCAATACCCAACACAGTGTATCCTGCCCAAGGACAGTGGCCAGCTCCAGTGAC
CAAACAGCCAGATATTAAGAACCCCAAGCTCACTAAGGATCAACAAACCACAGGGAGTCCCTCAAGAAAAA
CAATTACAATTACTGTGAAGTCTGTACCTCTGATACCATTCATATCTCTTGGAACCTTGCTCTACCTATG
ACTGCTTTGAGACTCAGCTGGCTTAACTGGGCCATAGCCCGGCATTTGGATCTATAACAGAAACAATTGT
AACAGGGGAACGCAGTGAGTACTTGGTCACAGCCCTGGAGCCTGATTCAACCCTATAAAGTATGCATGGTTC
CCATGGAAACCAGCAACCTCTACCTATTTGATGAACTCCTGTTTGTATTGAGACTGAACTGCACCCCTT
CGAATGTACAACCCTACAACCACCTCAATCGAGAGCAAGAGAAAGAACCTTACAAAAACCCCAATTACC
TTTGGCTGCCATCATTGGTGGGGCTGTGGCCCTGGTTACCATTGCCCTTCTTGCTTTAGTGTGTGGTATG
TTCATAGGAATGGATCGCTCTTCTCAAGGAACCTGTGCATATAGCAAAGGGAGGAGAAGAAAGGATGACTAT
GCAGAAGCTGGCACTAAGAAGGACAACCTCTATCCTGGAAATCAGGGAAACTTCTTTTCAGATGTTACCAAT
AAGCAATGAACCATCTCGAAGGAGGAGTTGTAATACACACCATATTTCTCCTAATGGAATGAATCTGT
ACAAAAACAATCAGAGTGAAGCAGTAGTAACCGAAGCTACAGAGACAGTGGTATTCAGACTCAGATCAC
TCACACTCATGATGCTGAAGGACTCACAGCAGACTTGTGTTTTGGGTTTTTTAAACCTAAGGGAGGTGATG
GT

FIGURE 132

MISAAWSIFLIGTKIGLFLQVAPLSVMAKSCPSVCRC DAGFIYCND RFLTSIPTGIPEDATTLYL
QNNQINNAGIPSDLKNLLKVERIYLYHNSLDEFPTNL PKYVKELHLQENNIR TITYDSL SKIPYL
EELHLD DNSVS AVSIEGA FRDSNYLRLLF LSRNHLSTIPWGLPRTIEELRLDDNRISTISSPSL
QGLTSLKRLVLDGNLLNNHGLGDKVFFNLVNLTELSLVRNSLT AAPVNLPGTNLRKLYLQDNHIN
RVPPNAFSYLRQLYRLDMSNNNLSNLPQGI FDDL DNITQLILRNNPWYCGCKMKWVRDWLQSLPV
KVNVRGLMCQAPEKVRGMAIKDLNAELFDC KDSGIVSTIQITTAIPNTVYPAQGQWPAPVTKQPD
IKNPKLTKDQQTGSPSRKTITITVKS VTS DTHISWKLALPMTALRLSWLKLGHSPA FGSITET
IVTGERSEYLVTALEPDSPYKVCMPMETSNLYL FDETPVC IETETAPLRMYNPTTTLNREQEKE
PYKNPNLPLAAIIGGAVALVTIAL LALVCWYVHRNGSLFSRNCAYSKGRRRKDDYAEAGTKKDNS
ILEIRETSFQMLPISNEPISKEEFVIHTIFPPNGMNL YKNNHSESSSNRSYRDSGIPDSDHSHS

Important features of the protein:

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 531-552

N-glycosylation sites.

amino acids 226-229, 282-285, 296-299, 555-558, 626-629, 633-636

Tyrosine kinase phosphorylation site.

amino acids 515-522

N-myristoylation sites.

amino acids 12-17, 172-177, 208-213, 359-364, 534-539, 556-561,
640-645

Amidation site.

amino acids 567-570

Leucine zipper pattern.

amino acids 159-180

Phospholipase A2 aspartic acid active site.

amino acids 34-44

FIGURE 133

CCGTCATCCCCCTGCAGCCACCCTTCCCAGAGTCCTTTGCCAGGCCACCCAGGCTTCTTGGCA
GCCCTGCCGGGCCACTTGTCTTCAATGTCTGCCAGGGGGAGGTGGGAAGGAGGTGGGAGGAGGGCG
TGCAGAGGCAGTCTGGGCTTGGCCAGAGCTCAGGGTGCTGAGCGTGTGACCAGCAGTGAGCAGAG
GCCGGCCATGGCCAGCCTGGGGCTGCTGCTCCTGCTCTTACTGACAGCACTGCCACCGCTGTGGT
CCTCCTCACTGCCTGGGCTGGACACTGCTGAAAGTAAAGCCACCATTGCAGACCTGATCCTGTCT
GCGCTGGAGAGAGCCACCGTCTTCTAGAACAGAGGCTGCCTGAAATCAACCTGGATGGCATGGT
GGGGGTCCGAGTGCTGGAAGAGCAGCTAAAAAGTGTCGGGAGAAGTGGGCCCAGGAGCCCTGC
TGCAGCCGCTGAGCCTGCGCGTGGGGATGCTGGGGAGAAGCTGGAAGCTGCCATCCAGAGATCC
CTCCACTACCTCAAGCTGAGTGATCCCAAGTACCTAAGAGAGTTCCAGCTGACCCTCCAGCCCGG
GTTTTGGAAGCTCCACATGCCTGGATCCACACTGATGCCCTCCTTGGTGTACCCACGTTCCGGGC
CCCAGGACTCATTCTCAGAGGAGAGAAGTGACGTGTGCCTGGTGCAGCTGCTGGGAACCGGACG
GACAGCAGCGAGCCCTGCGGCCTCTCAGACCTCTGCAGGAGCCTCATGACCAAGCCCGGCTGCTC
AGGCTACTGCCTGTCCACCAACTGCTCTTCTCTCTGGGCCAGAATGAGGGGATGCACACAGG
GACCACTCCAACAGAGCCAGGACTATATCAACCTCTTCTGCGCCAACATGATGGACTTGAACCGC
AGAGCTGAGGCCATCGGATACGCCTACCCTACCCGGGACATCTTCATGGAAAACATCATGTTCTG
TGGAATGGGCGGCTTCTCCGACTTCTACAAGCTCCGGTGGCTGGAGGCCATTCTCAGCTGGCAGA
AACAGCAGGAAGGATGCTTCGGGGAGCCTGATGCTGAAGATGAAGAATTATCTAAAGCTATTCAA
TATCAGCAGCATTTTTTCGAGGAGAGTGAAGAGGCGAGAAAAACAATTCCAGATTCTCGCTCTGT
TGCTCAGGCTGGAGTACAGTGGCGCAATCTCGGCTCACTGCAACCTTTCCTCTGGGTTCAGC
AATTCTCTTGCTCATCTTCCGAGTAGCTGGGACTACAGGAGCGTGCCACCATACTGGCTAAT
TTTTATATTTTTTTAGTAGAGACAGGGTTTCATCATGTTGCTCATGCTGGTCTCGAACTCCTGAT
CTCAAGAGATCCGCCCACCTCAGGCTCCCAAAGTGTTGGATTATAGTGTGAGCCACCGTGTCTG
GCTGAAAAGCACTTTCAAAGAGACTGTGTTGAATAAAGGGCCAAGGTTCTTGCCACCCAGCACTC
ATGGGGGCTCTCTCCCCTAGATGGCTGCTCCTCCCAACACAGCCACAGCAGTGGCAGCCCTGG
GTGGCTTCCATACATCTTGGCAGAATACCCCCAGCAAACAGAGAGCCACACCATCCACACCG
CCACCACCAAGCAGCGCTGAGACGACGGTTCATGCCAGCTGCCTGGAGGAGGAACAGACCCC
TTTAGTCCTCATCCCTTAGATCCTGGAGGGCACGGATCACATCCTGGGAAGAAGGCATCTGGAGG
ATAAGCAAAGCCACCCGACACCAATCTTGAAGCCCTGAGTAGGCAGGGCCAGGGTAGTGGG
GGCCGGGAGGGACCCAGGTGTGAACGGATGAATAAAGTTCAACTGCAACTGAAAAAAAAA

FIGURE 135

GGTCTGAGTGCAGAGCTGCTGTCAATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGCTG
CTGCTGCTATCGGGGGATGTCCAGAGCTCGGAGGTGCCGGGGCTGCTGCTGAGGGATCGGGAGG
GAGTGGGGTCGGCATAGGAGATCGCTTCAAGATTGAGGGCGTGCAATTGTTCCAGGGGTGAAGC
CTCAGGACTGGATCTCGGCGCCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTTTCTTTAAG
ACAGATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGGAAGTTGTATCTCC
AGCTTACAGATTTGATCCCGTTCGAGTGGATATCACTTCGAAAGGAAAAATGAGAGCAAGATATG
TGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAATGAAATCTTCAGGT
CCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTTCTAATGAACCCAATGGT
TATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCTAAAGTGGTCAACACAAGTGATC
CTGACATGAGACGGGAAATGGAGCAGTCAATGAATATGCTGAATTCCAACCATGAGTTGCCTGAT
GTTTCTGAGTTCATGACAAGACTCTTCTCTTCAAAATCATCTGGCAAATCTAGCAGCGGCAGCAG
TAAACAGGCAAAAGTGGGGCTGGCAAAGGAGGTAGTCAGGCCGTCCAGAGCTGGCATTTCAC
AAACACGGCAACACTGGGTGGCATCCAAGTCTTGGAACCCGTGTGAAGCAACTACTATAAACTT
GAGTCATCCCGACGTTGATCTCTTACAACCTGTGTATGTT
AACTTTTTAGCACATGTTTTGTACTTGGTACACGAGAAAACCCAGCTTTCATCTTTTGTCTGTAT
GAGGTCAATATTGATGTCACCTGAATTAATTACAGTGTCTTATAGAAAATGCCATTAATAAATTAT
ATGAACTACTATACATTATGTATATTAATTAACATCTTAATCCAGAAATCAAAAAAAAAAAAAA
AAAAAAAAAAAAAA

FIGURE 136

MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPDWISAA
 RVLVDGEEHVGFLLKTDGSEFVVDIPSGSYVVEVSPAYRFDVPRVDITSKGKMRARYVNYIKTSE
 VVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMVLPLLI FVLLPKVVNTSDPDMRREME
 QSMNMLNSNHELDPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGKRR

Important features of the protein:

Signal sequence:

amino acids 1-23

Transmembrane domain:

amino acids 161-182

N-glycosylation site.

amino acids 184-187

Glycosaminoglycan attachment sites.

amino acids 37-40, 236-239

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 151-154

N-myristoylation sites.

amino acids 33-38, 36-41, 38-44, 229-234

Amidation site.

amino acids 238-241

ATP/GTP-binding site motif A (P-loop).

amino acids 229-236

FIGURE 137

GATGGCGCAGCCACAGCTTCTGTGAGATTTCGATTTCTCCCCAGTTCCCCTGTGGGTCTGAGGGGA
 CCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATTCCTCCCAAAACAA
 GTTTTGACATTTCCCCTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCCTGCTGTTCAGGC
 CTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGCCACGACCTGTGC
 CACCAACTCGCACTCAGACTCTGAACTCAGACCTGAAATCTTCTCTTACGGGAGGCTTGGCAGT
 TTTTCTTACTCCTGTGGTCTCCAGATTTTCAGGCCTAAGATGAAAGCCTCTAGTCTTGCCTTCAGC
 CTCTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGGACTGAAGACACTCAATTTGGG
 AAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCTGAGATACGGGGCAGTG
 TGCAAGCCAAAGATGGAACATTGACATCAGAATCTTAAGGAGGACTGAGTCTTTGCAAGACACA
 AAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTTGCTAAGACTCTATCTGGACAGGGTATTTAA
 AAATACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGCAGCCTCGCCAATTCCTTTCTTA
 CCATCAAGAAGGACCTCCGGCTCTCTCATGCCACATGACATGCCATTGTGGGGAGGAAGCAATG
 AAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTGGAACCTCAGGCAGCAGTTGTGAAGGC
 TTTGGGGGAAGTAGACATTCTTCTGCAATGGATGGAGGAGACAGAATAGGAGGAAAGTGATGCTG
 CTGCTAAGAATATTGAGGTCAAGAGCTCCAGTCTTCAATACCTGCAGAGGAGGCATGACCCCAA
 ACCACCATCTCTTTACTGTACTAGTCTTGTGCTGGTCACAGTGTATCTTATTTATGCATTACTTG
 CTTCTTGCATGATTGTCTTTATGCATCCCCAATCTTAATTGAGACCATACTTGTATAAGATTTT
 TGTAATATCTTTCTGCTATTGGATATATTTATTAGTTAATATATTTATTTATTTTTTGGCTATTTA
 ATGTATTTATTTTTTACTTGGACATGAACTTTAAAAAAATTCACAGATTATATTTATAACCTG
 ACTAGAGCAGGTGATGTATTTTTTATACAGTAAAAAAAACCTTGTAATTTCTAGAAGAGTGG
 CTAGGGGGGTATTTCATTTGTATTCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGAT
 ATTTGAAATTGAACCAATGACTACTTAGGATGGGTGTGGAATAAGTTTGTGTGGAATTGCAC
 ATCTACCTTACAATTACTGACCATCCCCAGTAGACTCCCCAGTCCCATAATTGTGTATCTTCCAG
 CCAGGAATCCTACACGGCCAGCATGTATTTCTACAAATAAAGTTTCTTTGCATACCAAAAAAAA
 AAAAAAAAAA

FIGURE 138

MRQFPKTSFDISPEMSFSIYSLQVPAVPGLTCWALTAEPGWGQNKGATTCATNSHSDSELRPEIF
 SSREAWQFFLLLWSPDFRPMKASSLAFSLLSAFYLLWTPSTGLKTLNLGSCVIATNLQEIRNG
 FSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKIS
 SLANSFLTIIKDLRLSHAHTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEET
 E

Important features of the protein:

Signal peptide:

amino acids 1-42

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 192-195, 225-228

N-myristoylation sites.

amino acids 42-47, 46-51, 136-141

FIGURE 139

FIGURE 140

MRLGSGTFATCCVAIEVLGIAVFLRGFFPAPVRSSARAEGAEPPAPEPSAGASSNWTTLPPPLF
SKVVIVLIDALRDDVFVFGSKGVKFMPTTYLVEKGASHSFVAEAKPPTVTMPRIKALMTGSLPGF
VDVIRNLNSPALLEDVIRQAKAAGKRIVFYGDETWVKLFPKHFVEYDGTTSEFFVSDYTEVDNNV
TRHLDKVLKRGDWDILILHYLGLDGHIGHISGPN SPLIGQKLSEMDSVLMKIHTSLQSKERETPLP
NLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKPGDIRHPKHVQ

Important features of the protein:

Signal peptide:

amino acids 1-34

Transmembrane domain:

amino acids 58-76

N-glycosylation sites.

amino acids 56-60, 194-198

N-myristoylation sites.

amino acids 6-12, 52-58, 100-106, 125-131, 233-239, 270-276,
275-281, 278-284

Amidation site.

amino acids 154-158

Cell attachment sequence.

amino acids 205-208

FIGURE 141

GGCACGAGGCAAGCCTTCCAGGTTATCGTGACGCACCTTGAAAGTCTGAGAGCTACTGCCCTACA
GAAAGTTACTAGTGCCCTAAAGCTGGCGCTGGCACTGATGTTACTGCTGCTGTTGGAGTACAAC
TCCCTATAGAAAACAAC TGCCAGCACCTTAAGACCACTCACACCTTCAGAGTGAAGAACTTAAAC
CCGAAGAAATTCAGCATTTCATGACCAGGATCACAAAGTACTGGTCCTGGACTCTGGGAATCTCAT
AGCAGTTCAGATAAAAACTACATACGCCCAGAGATCTTCTTTGCATTAGCCTCATCCTTGAGCT
CAGCCTCTGCGGAGAAAGGAAGTCCGATTCTCCTGGGGGTCTCTAAAGGGGAGTTTTGTCTCTAC
TGTGACAAGGATAAAGGACAAAGTCATCCATCCCTTCAGCTGAAGAAGGAGAACTGATGAAGCT
GGCTGCCCCAAAAGGAATCAGCACGCCGGCCCTTCATCTTTTATAGGGCTCAGGTGGGCTCCTGGA
ACATGCTGGAGTCGGCGGCTCACCCCGGATGGTTCATCTGCACCTCCTGCAATTGTAATGAGCCT
GTTGGGGTGACAGATAAATTTGAGAACAGGAAACACATTGAATTTTCATTCAACCAGTTTGCAA
AGCTGAAATGAGCCCCAGTGAGGTCAGCGATTAGGAAACTGCCCCATTGAACGCCTTCCTCGCTA
ATTTGAACTAATTGTATAAAAAACCAAACCTGCTCACT

FIGURE 142

MLLLLLLEYNFPIENNCQHLKTTHTFRVKNLNPKKFSIHDQDHKVLVLDSGNLIAVPDKNYIRPEI
FFALASSLSSASAEKGSPILLGVSKGEFCLYCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFI
FYRAQVGSWNMLESAAHPGWFICTSCNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD

cAMP- and cGMP-dependent protein kinase phosphorylation site.
amino acids 33-36

N-myristoylation site.
amino acids 50-55, 87-92

Interleukin-1
amino acids 37-182

FIGURE 143

CTAGAGAGTATAGGGCAGAAGGATGGCAGATGAGTGACTCCACATCCAGAGCTGCCTCCCTTTAA
TCCAGGATCCTGTCTTCCTGTCTGTAGGAGTGCCGTGTGCCAGTGTGGGGTGAGACAAGTTTG
TCCCACAGGGCTGTCTGAGCAGATAAGATTAAGGGCTGGGTCTGTGCTCAATTAACCTGTGGG
CACGGGGGCTGGGAAGAGCAAAGTCAGCGGTGCCTACAGTCAGCACCATTGCTGGGCCTGCCGTGG
AAGGGAGGTCTGTCTGGGCGCTGCTGCTGCTTCTCTTAGGCTCCCAGATCCTGTGATCTATGC
CTGGCATTTCACGAGCAAAGGACTGTGATGAACACAATGTCATGGCTCGTTACCTCCCTGCCA
CAGTGGAGTTTGCTGTCCACACATTCAACCAACAGAGCAAGGACTACTATGCCTACAGACTGGGG
CACATCTTGAATTCCTGGAAGGAGCAGGTGGAGTCCAAGACTGTATTCTCAATGGAGCTACTGCT
GGGGAGAACTAGGTGTGGGAAATTTGAAGACGACATTGACAACTGCCATTTCCAAGAAAGCACAG
AGCTGAACAATACTTTCACCTGCTTCTTCACCATCAGCACCCAGGCCCTGGATGACTCAGTTCAGC
CTCCTGAACAAGACCTGCTTGGAGGGATTCCACTTGAGTGAAACCCACTCACAGGCTTGTCATGT
GCTGCTCCACATTCCGTGGACATCAGCACTACTCTCCTGAGGACTCTTCAGTGGCTGAGCAGCT
TTGGACTTGTTTGTATCCTATTTTGCATGTGTTTGAGATCTCAGATCAGTGTTTTAGAAAAATCC
ACACATCTTGAGCCTAATCATGTAGTGTAGATCATTAAACATCAGCATTTTAAGAAAAAAAAAAAA
AA

FIGURE 144

MLGLPWKGGLSWALLLLLLLGSQILLIYAWHFHEQRDCDEHNVMARYLPATVEFAVHTFNQQSKDY
YAYRLGHILNSWKEQVESKTVFSMELLLGRTRCGKFEDDIDNCHFQESTELNNTFTCFFTISTRP
WMTQFSLLNKTCLEGFH

Important features of the protein:

Signal peptide:

amino acids 1-25

N-glycosylation sites.

amino acids 117-121, 139-143

N-myristoylation site.

amino acids 9-15

FIGURE 145

CACCTGAGCTGGTGGTGGCTGGCCACTGTCTGCATGCTGCTCTTCAGCCACCTCTCTGCGGTCCA
 GACGAGGGGCATCAAGCACAGAATCAAGTGAACCGGAAGGCCCTGCCAGCACTGCCAGATCA
 CTGAGGCCCAGGTGGCTGAGAACCGCCCGGGAGCCTTCATCAAGCAAGGCCGCAAGCTCGACATT
 GACTTCGGAGCCGAGGGCAACAGGTACTACGAGGCCAACTACTGGCAGTTCCTCCGATGGCATCCA
 CTACAACGGCTGCTCTGAGGCTAATGTGACCAAGGAGGCATTTGTACCCGGCTGCATCAATGCCA
 CCCAGGCGGCGAACCAGGGGAGTTCCAGAAGCCAGACAACAAGTCCACCAGCAGGTGCTCTGG
 CGGCTGGTCCAGGAGCTCTGCTCCCTCAAGCATTGCGAGTTTTGGTTGGAGAGGGGCGCAGGACT
 TCGGGTCACCATGCACCAGCCAGTGCTCCTCTGCCTTCTGGCTTTGATCTGGCTCATGGTGAAAT
AAGCTTGCCAGGAGGCTGGCAGTACAGAGCGCAGCAGCGAGCAAATCCTGGCAAGTGACCCAGCT
 CTTCTCCCCCAAACCCACGCGTGTCTGAAGGTGCCAGGAGCGCGATGCACTCGCACTGCAAA
 TGCCGCTCCCACGTATGCGCCCTGGTATGTGCCTGCGTTCTGATAGATGGGGGACTGTGGCTTCT
 CCGTCACTCCATTCTCAGCCCCCTAGCAGAGCGTCTGGCACACTAGATTAGTAGTAAATGCTTGAT
 GAGAAGAACACATCAGGCACTGCGCCACCTGCTTCACAGTACTTCCCAACAACCTCTTAGAGGTAG
 GTGTATTCCCGTTTTACAGATAAGGAAACTGAGGCCCGAGAGCTGAAGTACTGCACCCAGCATC
 ACCAGCTAGAAAGTGGCAGAGCCAGGATTCAACCCTGGCTTGTCTAACCCAGGTTTTCTGCTCT
 GTCCAATTCCAGAGCTGTCTGGTGATCACTTTATGTCTCACAGGGACCCACATCCAAACATGTAT
 CTCTAATGAAATTGTGAAAGCTCCATGTTTAGAAATAAATGAAAACACCTGA

FIGURE 146

MRKHLSSWWLATVCMLLFSHLSAVQTRGIKHKRIKWNRKALPSTAQITEAQVAENRPGAFIKQGRK
LDIDFGAEGNRYYEANYWQFPDGIHYNGCSEANVTKEAFVTGCINATQAAHQGEFQKPDNKLHQQ
VLWRLVQELCSLKHCEFWLERGAGLRVTMHQPVLLCLLALIWLMVK

Important features of the protein:

Signal peptide:

amino acids 1-26

Transmembrane domain:

amino acids 157-171

N-glycosylation sites.

amino acids 98-102, 110-114

Tyrosine kinase phosphorylation site.

amino acids 76-83

N-myristoylation sites.

amino acids 71-77, 88-94, 93-99, 107-113, 154-160

Amidation site.

amino acids 62-66

[illegible]

MFRSSLLFWPPLCLLSLFLILISSIYESCKLEIFHFACQWGRSLSLSFYFLKFQLSDSGGTCE
GLFYEYIA

Important features of the protein:

Signal peptide:

amino acids 1-25

N-myristoylation site.

amino acids 62-68

FIGURE 149

GTCTCCGCGTCACAGGAACCTTCAGCACCCACAGGGCGGACAGCGCTCCCTCTACCTGGAGACTTGAC
TCCCGCGCGCCCCAACCCCTGCTTATCCCTTGACCGTCGAGTGTTCAGAGATCCTGCAGCCGCCCCAGTCC
CGGCCCCCTCTCCCGCCCCACACCCACCCCTCCTGGCTCTTCTGTTTTACTCTCTCTTTTCATTTCATA
ACAAAAGCTACAGCTCCAGGAGCCAGCGCCGGGCTGTGACCCAAGCCGAGCGTGGAAGAATGGGGT
CCTCGGGACCGGCACTTGGATTCTGGTGTAGTGCTCCCGATTCAAGCTTTCCCAACCTGGAGGAA
GCCAAGACAAATCTCTACATAATAGAGAATTAAGTGCAGAAAGACCTTTGAATGAACAGATTGCTGAA
GCAGAAGAAGACAAGATTAAAAAACATATCCTCCAGAAAACAAGCCAGGTTCAGAGCAACTATTCTTT
TGTGATAACTTGAACCTGCTAAAGGCAATAACAGAAAAGGAAAAATTGAGAAAGAAAGACAATCTA
TAAGAAGCTCCCCACTTGATAATAAGTTGAATGTGGAAGATGTTGATTCAACCAAGAATCGAAAACTG
ATCGATGATTATGACTCTACTAAGAGTGGATTGGATCATAAATTTCAAGATGATCCAGATGGTCTTCA
TCAACTAGACGGGACTCCTTTAACCCTGTAAGACATTGTCCATAAAATCGTGCAGGATTTATGAAG
AAAATGACAGAGCCGTGTTTGACAAGATTGTTCTAACTACTTAATCTCGGCCTTATCACAGAAAGC
CAAGCACATACACTGGAAGATGAAGTAGCAGAGGTTTTACAAAAATTAATCTCAAAGGAAGCCAACAA
TTATGAGGAGGATCCCAATAAGCCCAAGCTGGACTGAGAATCAGGCTGGAAAAATACCAGAGAAAG
TGACTCCAATGGCAGCAATTCAAGATGGTCTTGCTAAGGGAGAAAACGATGAAACAGTATCTAACACA
TTAACCTTGACAAATGGCTTGGAAGGAGAACTAAAACCTACAGTGAAGACAACCTTTGAGGAACCTCA
ATATTTCCCAAATTTCTATGCGCTACTGAAAAGTATTGATTGAGAAAAGAAGCAAAAGAGAAAGAAA
CACTGATTACTATCATGAAAACACTGATTGACTTTGTGAAGATGATGGTGAATATGGAACAATATCT
CCAGAAGAAGGTGTTTCTACCTTGAAAACCTGGATGAAATGATTGCTCTTCAGACCAAAAACAAGCT
AGAAAAAATGCTACTGACAATATAAGCAAGCTTTTCCAGCACCATCAGAGAAGAGTCATGAAGAAA
CAGACAGTACCAAGGAAGAAGCAGCTAAGATGGAAGGAATATGGAAGCTTGAAGGATTCCACAAAA
GATGATAACTCCAACCCAGGAGGAAAGACAGATGAACCCAAAGGAAAAACAGAAGCCTATTTGGAAGC
CATCAGAAAAAATATGAATGGTTGAAGAAACATGACAAAAAGGAAATAAAGAAGATTATGACCTTT
CAAAGATGAGAGACTTCATCAATAAACAAGCTGATGCTTATGTGGAGAAAGGCATCCTTGACAAGGAA
GAAGCCGAGGCCATCAAGCGCATTTATAGCAGCCTGTAAAAATGGCAAAAGATCCAGGAGTCTTTCAA
CTGTTTCAGAAAACATAATATAGCTTAAACACTTCTAATCTGTGATTAAAATTTTTTGACCCAAGG
GTTATTAGAAAGTGCTGAATTTACAGTAGTTAACCTTTTACAAGTGGTTAAACATAGCTTTCTTCCC
GTAAAAACTATCTGAAAGTAAAGTTGTATGTAAGCTGAAAAAAGAAAAAAGAAAAA

FIGURE 150

MGFLGTGTWILVLVLP IQAFPKPGGSQDKSLHNRELSAERPLNEQIAEAEEDKIKKTYPPENKPG
 QSNYSFVDNLNLLKAITEKEKIEKERQSIRSSPLDNKLNVEDVDSTKNRKLIDYDSTKSGLDHK
 FQDDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDEVAE
 VLQKLISKEANNYEEDPNKPTSWTENQAGKIPKVTMAAIQDGLAKGENDETVSNTLTLTNGLE
 RRTKTYSEDNFEELQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKMMVKYGTISPEEGV
 SYLENLDEMIALQTKNKLEKNATDNISKLFAPSEKSHEETDSTKEEAAKMEKEYGSLKDSTKDD
 NSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYDLSKMRDFINKQADAYVEKGILDK
 EEAEAIKRIYSSL

N-glycosylation sites:

amino acids 68-71, 346-349, 350-353

Casein kinase II phosphorylation site:

amino acids 70-73, 82-85, 97-100, 125-128, 147-150, 188-191, 217-
 220, 265-268, 289-292, 305-308, 320-323, 326-329, 362-365, 368-
 341, 369-372, 382-385, 386-389, 387-390

N-myristoylation sites:

amino acids 143-148, 239-244

FIGURE 151

CGGCTCGAGGCTCCCGCCAGGAGAAAGGAACATTCTGAGGGGAGTCTACACCCTGTGGAGCTCAA
GATGGTCCTGAGTGGGGCGCTGTGCTTCCGAATGAAGGACTCGGCATTGAAGGTGCTTTATCTGC
 ATAATAACCAAGCTTCTAGCTGGAGGGCTGCATGCAGGGAAGGTCATTAAAGGTGAAGAGATCAGC
 GTGGTCCCCAATCGGTGGCTGGATGCCAGCCTGTCCCCCGTCATCCTGGGTGTCCAGGTGGAAG
 CCAGTGCCTGTCAATGTGGGGTGGGGCAGGAGCCGACTCTAACACTAGAGCCAGTGAACATCATGG
 AGCTCTATCTTGGTGCCAAGGAATCCAAGAGCTTACCTTCTACCGGCGGGACATGGGGCTCACC
 TCCAGCTTCGAGTCGGCTGCCTACCCGGGCTGGTTCCCTGTGCACGGTGCCTGAAGCCGATCAGCC
 TGTCAAGACTCACCCAGCTTCCCGAGAATGGTGGCTGGAATGCCCCCATCACAGACTTCTACTTCC
 AGCAGTGTGACTAGGGCAACGTGCCCCCAGAACTCCCTGGGCAGAGCCAGCTCGGGTGAGGGGT
 GAGTGGAGGAGACCCATGGCGGACAATCACTCTCTCTGCTCTCAGGACCCACAGTCTGACTTAG
 TGGGCACCTGACCACTTTGTCTTCTGGTTCCAGTTTGGATAAATTCTGAGATTTGGAGCTCAGT
 CCACGGTCCTCCCCCACTGGATGGTGTACTGTGTGGAACCTTGTA AAAACCATGTGGGGTAAA
 CTGGGAATAACATGAAAAGATTCTGTGGGGGTGGGGTGGGGGAGTGGTGGGAATCATTCTGTCT
 TAATGGTAAGTACAAAGTGTACCTGTAGCCCCGAGGCCAACCCATCCCCAGTTGAGCCTTATA
 GGGTCAGTAGCTCTCCACATGAAGTCTGTCACTCACCCTGTGCAGGAGAGGGAGGTGGTCATA
 GAGTCAGGGATCTATGGCCCTTGGCCCAAGCCCCACCCCTTCCCTTTAATCTGCACTGTCCATA
 TGCTACCTTTCCCTATCTCTTCCCTCATCATCTTGTGTGGGCATGAGGAGGTGGTGTATGTCAGAA
 GAAATGGCTCGAGCTCAGAAGATAAAAGATAAGTAGGGTATGCTGATCCTCTTTTAAAAACCCAA
 GATACAATCAAAATCCCAGATGCTGGTCTCTATTCCCATGAAAAAGTGTCTATGACATATTGAGA
 AGACCTACTTACAAAGTGGCATATATTGCAATTTATTTTAAATTAAGATACCTATTTATATATT
 TCTTTATAGAAAAAGTCTGGAAGAGTTTACTTCAATTGTAGCAATGTGAGGGTGGTGGCAGTAT
 AGGTGATTTTTCTTTAATTCTGTAAATTTATCTGTATTTCTAATTTTTCTACAATGAAGATGA
 ATTCCTTGTATAAAAAATAAGAAAAAGAAATTAATCTTGAGGTAAAGCAGAGCAGACATCTCTGA
 TTGCTCTCAGCCTCCACTTCCCCAGAGTAAATTCAAATTGAATCGAGCTCTGCTGCTCTGGTTGG
 TTGTAGTAGTGATCAGGAAACAGATCTCAGCAAAGCCACTGAGGAGGAGGCTGTGCTGAGTTTGT
 GTGGCTGGAATCTCTGGGTAAGGAACCTAAAGAACAAAAATCATCTGGTAATCTTTCCCTAGAAG
 GATCACAGCCCCCTGGGATTCCAAGGCATTGGATCCAGTCTCTAAGAAGGCTGCTGTACTGGTTGA
 ATTTGTGCCCCCTCAAATTCACATCCTTCTTGGAACTCTCAGTCTGTGAGTTTATTTGGAGATAAG
 GTCTCTGCAGATGTAGTTAGTTAAGACAAGGTCAATGCTGGATGAAGGTAGACCTAAATTCATAT
 GACTGGTTTCTTGTATGAAAAGGAGAGGACACAGAGACAGAGGAGACGCGGGGAAGACTATGTA
 AAGATGAAGGCAGAGATCGGAGTTTTGCAGCCACAAGCTAAGAAACACCAAGGATTGTGGCAACC
 ATCAGAAGCTTGAAGAGGCAAGAAGAAATCTTCCCTAGAGGCTTTAGAGGGATAACGGCTCTG
 CTGAAACCTTAATCTCAGACTTCCAGCCTCCTGAACGAAGAAAGAAATAAATTTCCGGCTGTTTAA
 GCCACCAAGGATAAATTGGTTACAGCAGCTCTAGGAACTAATACAGCTGCTAAAAATGATCCCTGT
 CTCCTCGTGTTTACATTCTGTGTGTGTCCCCCTCCACAATGTACCAAAGTTGTCTTTGTGACCAA
 TAGAATATGGCAGAAGTGATGGCATGCCACTTCCAAGATTAGGTTATAAAAGACACTGCAGCTTC
 TACTTGAGCCCTCTCTCTCTGCCACCCACCGCCCCAATCTATCTTGGCTCACTCGCTCTGGGGG
 AAGCTAGCTGCCATGCTATGAGCAGGCCTATAAAGAGACTTACGTGGTAAAAAATGAAGTCTCCT
 GCCACAGCCACATTAGTGAACCTAGAAGCAGAGACTCTGTGAGATAATCGATGTTTGTGTTTT
 AAGTTGCTCAGTTTTGGTCTAACTTGTATGCAGCAATAGATAAATAATATGCAGAGAAAGAG

FIGURE 152

MVLSGALCFRMKDSALKVLYLHNNQLLAGGLHAGKVIKGEESISVVPNRWLDASLSPVILGVQGGG
QCLSCGVGQEPTLTLEPVNIMELYLGAKESKSFTFYRRDMGLTSSFESAAYPGWFLCTVPEADQP
VRLTQLPENGGWNAIPITDFYFQQCD

N-myristoylation sites.

amino acids 29-34, 30-35, 60-65, 63-68, 73-78, 91-96, 106-111

Interleukin-1 signature.

amino acids 111-131

Interleukin-1 proteins.

amino acids 8-29, 83-120, 95-134, 64-103

FIGURE 153

CTTCAGAACAGGTTCTCCTTCCCCAGTCACCAAGTTGCTCGAGTTAGAATTGTCTGCAATGGCCGC
 CCTGCAGAAATCTGTGAGCTCTTTCCTTATGGGGACCTGGCCACCAGCTGCCTCCTTCTCTTGG
 CCCTCTTGGTACAGGGAGGAGCAGCTGCGCCCATCAGCTCCCACTGCAGGCTTGACAAGTCCAAC
 TTCCAGCAGCCCTATATCACCACCGCACCTTCATGCTGGCTAAGGAGGCTAGCTTGGCTGATAA
 CAACACAGACGTTTCGTCTCATTGGGGAGAACTGTTCCACGGAGTCAGTATGAGTGAGCGCTGCT
 ATCTGATGAAGCAGGTGCTGAACTTCACCTTGAAGAAGTGCTGTTCCCTCAATCTGATAGGTTC
 CAGCCTTATATGCAGGAGGTGGTGCCCTTCCTGGCCAGGCTCAGCAACAGGCTAAGCACATGTCA
 TATTGAAGGTGATGACCTGCATATCCAGAGGAATGTGCAAAAGCTGAAGGACACAGTGAAAAAGC
 TTGGAGAGAGTGGAGAGATCAAAGCAATTGGAGAAGTGGATTGCTGTTTATGTCTCTGAGAAAT
 GCCTGCATTTGACCAGAGCAAAGCTGAAAAATGAATAACTAACCCCTTTCCCTGCTAGAAATAA
 CAATTAGATGCCCCAAAGCGATTTTTTTTAACCAAAGGAAGATGGGAAGCCAACTCCATCATG
 ATGGGTGGATTCCAAATGAACCCCTGCGTTAGTTACAAAGGAAACCAATGCCACTTTTGTTTATA
 AGACCAGAAGGTAGACTTTCTAAGCATAGATATTTATTGATAACATTTTCATTGTAAGTGGTGTTT
 TATACACAGAAAACAATTTATTTTTTAAATAATTGTCTTTTCCATAAAAAAGATTACTTTCCAT
 TCCTTTAGGGGAAAAAACCCCTAAATAGCTTCATGTTCCATAATCAGTACTTTATATTTATAAA
 TGTATTTATTATTATTATAAGACTGCATTTTATTATATCATTTTATTAATATGGATTTATTTAT
 AGAAACATCATTCGATATTGCTACTTGAGTGTAAGGCTAATATTGATATTTATGACAATAATTAT
 AGAGCTATAACATGTTTATTTGACCTCAATAAACACTTGGATATCCC

[illegible]

Important features of the protein:

amino acids 1-33

amino acids 54-58, 68-72, 97-101

amino acids 14-20, 82-88

amino acids 10-21

THE UNIVERSITY OF CHICAGO

APP ID=10063520

FIGURE 156

MRERPRLGEDSSLISLFLQVVAFLAMVMGTHYSHWPSCCPKSGQDTSEELLRWSTVPVPPEPA
RPNRHPESCRAEDGPLNSRAISPWRYELDRDLNRLPQDLYHARCLCPHCVSLQTGSHMDPRGNS
ELLYHNQTVFYRRPCHGEKGTHKGYCLERRLYRVSLACVCVRPRVMG

Important features of the protein:

Signal peptide:

amino acids 1-32

N-glycosylation site.

amino acids 136-140

Tyrosine kinase phosphorylation site.

amino acids 127-135

N-myristoylation sites.

amino acids 44-50, 150-156

FIGURE 157

CCGGCGATGTCGCTCGTGTGCTAAGCCTGGCCGCGCTGTGCAGGAGCGCCGTACCCCGAGAGCC
GACCGTTCAATGTGGCTCTGAACTGGGCCATCTCCAGAGTGGATGCTACAACATGATCTAATCC
CCGGAGACTTGAGGGACCTCCGAGTAGAACCTGTTACAACAGTGTGCAACAGGGGACTATTCA
ATTTTGATGAATGTAAGCTGGGTACTCCGGGCAGATGCCAGCATCCGCTTGTGAAGGCCACCAA
GATTGTGTGACGGGCAAAAGCAACTTCCAGTCTACAGCTGTGTGAGGTGCAATTACACAGAGG
CCTTCCAGACTCAGACCAGACCTCTGGTGGTAAATGGACATTTTCTACATCGGCTTCCCTGTA
GAGCTGAACACAGTCTATTTTCATTGGGGCCATAATATTCCTAATGCAAATATGAATGAAGATGG
CCCTTCCATGTCTGTGAATTTACCTCACCAGGCTGCCTAGACCACATAATGAAATATAAAAAA
AGTGTGTCAAGGCCGGAAGCCTGTGGGATCCGAACATCACTGCTTGAAGAAGATGAGGAGACA
GTAGAAGTGAACCTCACAACCACTCCCTGGGAAACAGATACATGGCTCTTATCCAACACAGCAC
TATCATCGGGTTTTCTCAGGTGTTTGAGCCACACCAGAAGAAACAAACGCGAGCTTCAGTGGTGA
TTCCAGTGAAGGATAGTGAAGGTGCTACGGTGCAGCTGACTCCATATTTTCTACTTGTGGC
AGCGACTGCATCCGACATAAAGGAACAGTTGTGCTCTGCCCCACAAACAGGCGTCCCTTTCCCTCT
GGATAACAACAAAAGCAAGCCGGGAGGCTGGCTGCCTCTCCTCTGCTGTCTCTGCTGGTGGCCA
CATGGGTGCTGGTGGCAGGGATCTATCTAATGTGGAGGCACGAAAGGATCAAGAAGACTTCCTTT
TCTACCACCACACTACTGCCCCCATTAAGGTTCTTGTGGTTTACCCATCTGAAATATGTTTCCA
TCACACAATTTGTTACTTCACTGAATTTCTTCAAACCAATTGCAGAAGTGAGGTGATCCTTGAAA
AGTGGCAGAAAAAGAAAATAGCAGAGATGGGTCCAGTGCAGTGGCTTGCCACTCAAAGAAGGCA
GCAGACAAAGTCGTCTTCCTTCTTTCCAATGACGTCAACAGTGTGTGCGATGGTACCTGTGGCAA
GAGCGAGGGCAGTCCAGTGAGAACTCTCAAGACCTCTTCCCCCTTGCCCTTTAACCTTTTCTGCA
GTGATCTAAGAAGCCAGATTATCTGCACAAATACGTGGTGGTCTACTTTAGAGAGATTGATACA
AAAGACGATTACAATGCTCTCAGTGTCTGCCCCAAGTACCACCTCATGAAGGATGCCACTGCTTT
CTGTGCAGAACTTCTCCATGTCAAGCAGCAGGTGTCAGCAGGAAAAAGATCACAAGCCTGCCACG
ATGGCTGCTGCTCCTTGTAG

FIGURE 159

AGCCACCAGCGCAACATGACAGTGAAGACCCTGCATGGCCCAGCCATGGTCAAGTACTTGCTGCT
GTCGATATTGGGGCTTGCCTTTCTGAGTGAGGCGGCAGCTCGGAAAATCCCCAAAGTAGGACATA
CTTTTTTCCAAAAGCCTGAGAGTTGCCCGCCTGTGCCAGGAGGTAGTATGAAGCTTGACATTGGC
ATCATCAATGAAAACCAGCGCGTTTCCATGTCACGTAACATCGAGAGCCGCTCCACCTCCCCCTG
GAATTACACTGTCACCTTGGGACCCCAACCGGTACCCCTCGGAAGTTGTACAGGCCCAGTGTAGGA
ACTTGGGCTGCATCAATGCTCAAGGAAAGGAAGACATCTCCATGAATTCCGTTCCCATCCAGCAA
GAGACCCTGGTCGTCCGGAGGAAGCACCAAGGCTGCTCTGTTTCTTTCCAGTTGGAGAAGGTGCT
GGTGACTGTTGGCTGCACCTGCGTCACCCCTGTCATCCACCATGTGCAGTTAAGAGGTGCATATCC
ACTCAGCTGAAGAAG

FIGURE 160

MTVKTLHGPMVKYILLLSILGLAFLSEAAARKIPKVGHTFFQKPESCPPVPGGSMKLDIGIINEN
QRVSMERNIESRSTSPWNYTWTWDPNRYPSSEVVQAQCRNLGCINAQKEDISMNSVPIQQETLVV
RRKHQGCSSVSFQLEKVLVTVGCTCVTPVIHHVQ

Signal sequence:

amino acids 1-30

N-glycosylation site.

amino acids 83-87

N-myristoylation sites.

amino acids 106-111, 136-141

FIGURE 161

ACACTGGCCAAACAAAAACGAAAGCACTCCGTGCTGGAAGTAGGAGGAGAGTCAGGACTCCCAGG
ACAGAGAGTGCACAACTACCCAGCACAGCCCCCTCCGCCCCCTCTGGAGGCTGAAGAGGGATT
CAGCCCCCTGCCACCCACAGACACGGGCTGACTGGGGTGTCTGCCCCCTTGGGGGGGGGAGCAC
AGGGCCTCAGGCCTGGGTGCCACCTGGCACCTAGAAGATGCCTGTGCCCTGGTTCTTGCTGTCT
TGGCACTGGGGCCGAAGCCAGTGGTCCTTTCTCTGGAGAGGCTTGTGGGGCCTCAGGACGCTACC
CACTGCTCTCCGGGCTCTCCTGCCGCTCTGGGACAGTGACATACTCTGCCTGCCTGGGGACAT
CGTGCTGCTCCGGGCCCCGTGCTGGCGCCTACGCACCTGCAGACAGAGCTGGTGCTGAGGTGCC
AGAAGGAGACCGACTGTGACCTCTGTCTGCGTGTGGCTGTCCACTTGGCCGTGCATGGGCACTGG
GAAGAGCCTGAAGATGAGGAAAAGTTTGGAGGAGCAGCTGACTCAGGGGTGAGGAGCCTAGGAA
TGCTCTCTCCAGGCCCAAGTCGTCTCTCCTTCCAGGCCTACCTACTGCCCCGTGCGTCTCTG
TGGAGGTGCAAGTGCTGCTGCCCTTGTGCACTTGGTCACTGTGGGGCTCTGTGGTATATGAC
TGCTTCGAGGCTGCCCTAGGGAGTGAGGTACGAATCTGGTCTTATACTCAGCCAGGTACAGAA
GGAACCAACACACACAGCAGCTGCCTGCCCTGCCCTGGCTCAACGTGTGAGCAGATGGTGACA
ACGTGCATCTGGTTCTGAATGTCTCTGAGGAGCAGCACTTCGGCCTCTCCCTGTACTGGAATCAG
GTCCAGGGCCCCCAAAACCCCGTGGCACAAAAACCTGACTGGACCGCAGATCATTACCTTGAA
CCACACAGACCTGGTTCCCTGCCCTCTGTATTTCAGGTGTGGCCTCTGGAACCTGACTCCGTTAGGA
CGAACATCTGCCCCCTCAGGGAGGACCCCGCGCACACCAGAACCTCTGGCAAGCCGCCCCGACTG
CGACTGCTGACCCTGCAGAGCTGGCTGCTGGACGACCGTGTCTGCTGCCCCGAGAAGCGGCACT
GTGCTGGCGGGCTCCGGGTGGGGACCCCTGCCAGCCTGGTCCCACCGCTTTCCTGGGAGAAGC
TCACTGTGGACAAGTTCTCGAGTTCCCATTGCTGAAAGGCCACCCTAACCTCTGTGTTTCAAGTG
AACAGCTCGGAGAAGCTGCAGCTGCAGGAGTGCTTGTGGGCTGACTCCCTGGGGCCTCTCAAAGA
CGATGTGCTACTGTGGAGACACGAGGCCCCAGGACAACAGATCCCTCTGTGCCCTTGAACCCA
GTGGCTGTACTTCACTACCCAGCAAAGCCTCCACGAGGGCAGCTCGCCTTGAGAGTACTTACTA
CAAGACCTGCAGTCAGGCCAGTGTCTGCAGCTATGGGACGATGACTTGGGAGCGCTATGGGCCTG
CCCCATGGACAAATACATCCACAAGCGCTGGGCCCTCGTGTGGCTGGCCTGCCTACTCTTTGCCG
CTGCGCTTTCCCTCATCCTCCTTCTCAAAAAGGATCACGCGAAAGGGTGGCTGAGGCTCTTGAAA
CAGGACGTCCGCTCGGGGGCGGCCGCCAGGGGGCGCGCGCTGTCTCCTTACTCAGCCGATGA
CTCGGGTTTCGAGCGCTGGTGGGCGCCCTGGCGTCCGGCCTGTGCCAGCTGCCGCTGCGCGTGG
CCGTAGACCTGTGGAGCCGTCTGTGAAGTGAAGCGCGCAGGGGCCCTGGCTTGGTTTACGCGCAG
CGGCGCCAGACCTGCAGGAGGGCGGCGTGGTGGTCTTGTCTTCTCTCCCGGTGCGGTGGCGCT
GTGACGAGTGGCTACAGGATGGGGTGTCCGGGGCCGGGGCGCACGGCCCGACGACGCTTCC
GCGCCTCGCTCAGTGTGCTGCTGCGGACTTCTTTCAGGGCCGGGCGCCCGGCGAGCTACGTGGGG
GCCTGCTTCGACAGGCTGTCTCCACCCGACGCCGTACCCGCCCTTTCCGACCGTGCCCGTCTT
CACACTGCCCTCCCACTGCCAGACTTCTTGGGGGCCCTGCAGCAGCCTCGCGCCCCGCGTTCCG
GGCGGCTCCAAGAGAGAGCGGAGCAAGTGTCCCGGGCCCTTACGCCAGCCTGGATAGCTACTTC
CATCCCCCGGGGACTCCCGCGCGGGACGCGGGGTGGGACCAGGGGCGGGACCTGGGGCGGGGA
CGGGACTTAAATAAAGGCAGACGCTGTTTTCTAAAAAA

FIGURE 162

MPVPWFLLSLALGRSPVVLSELERLVGPQDATHCSEGLSCLWDSILCLPGDIVPAPGPVLAPTHLQTELV
LRCQKETDCDLCLRVAVHLAVHGHWEPEDEEKFGGAADSGVEEPRNASLQAQVVLSTFQAYPTARCVLLEV
QVPAALVQFGQSVGSGVVDCEAALGSEVRIWSYTQPRYEKELNHTQQLPALPWLNVSAADGNVHLVLNV
EEQHFGSLYWNQVQGPPKPRWHKNLTGPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQ
LWQAARLRLTLQSWLLDAPCSLPAEAALCWRAPGGDPCQLVPPLSWENVTVDKVLEFPLLKGHPNLCVQ
VNSSEKLQEQECLWADSLGPKDDVLLLETRGPQDNRSLEPSGCTSLPSKASTRAARLGEYLLQDLQS
GQCLQLWDDDLGALWACPMKYIHKRWALVWLACLLFAAALSLILLKKDHAKGWLRLKQDVRSGAAARG
RAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELSAQGPVAVFHAQRRQTLQEGGVVLLFSP
GAVALCSEWLQDGVSGPGAHGPHDAFRASLSCVLPDFLQGRAPGSYVGACFDRLHHPDAVPALFRTVPVFT
LPSQLPDFLGALQQPRAPRSGRLQERAEQVSRAALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT

Signal sequence:
amino acids 1-20

Transmembrane domain.
amino acids 453-475

N-glycosylation sites.
amino acids 118-121, 186-189, 198-201, 211-214, 238-241, 248-251,
334-337, 357-360, 391-394

Glycosaminoglycan attachment site.
amino acids 583-586

cAMP- and cGMP-dependent protein kinase phosphorylation site.
amino acids 552-555

N-myristoylation sites.
amino acids 107-112, 152-157, 319-324, 438-443, 516-521, 612-617,
692-697, 696-701, 700-705

FIGURE 163

GGGAGGGCTCTGTGCCAGCCCCATGAGGACGCTGCTGACCATCTTGACTGTGGGATCCCTGGCT
GCTCAGCCCCCTGAGGACCCCTCGGATCTGCTCCAGCACGTGAAATTCCAGTCCAGCAACTTTGA
AAACATCCTGACGTGGGACAGCGGGCCAGAGGGCACCCAGACACGGTCTACAGCATCGAGTATA
AGACGTACGGAGAGAGGGACTGGGTGGCAAAGAAGGGCTGTCAGCGGATCACCCGGAAGTCTGC
AACCTGACGGTGGAGACGGGCAACCTCACGGAGCTCTACTATGCCAGGGTCACCGCT
GTCAGTGCGGGAGGCGGTGAGCCACCAAGATGACTGACAGGTTGAGCTCTCTGCAGCACACTAC
CCTCAAGCCACCTGATGTGACCTGTATCTCCAAAGTGAGATCGATTTCAGATGATTGTTTCATCCTA
CCCCACGCCAATCCGTGCAGGCGATGGCCACCGGCTAACCTTGAAGACATCTTCCATGACCTG
TTCTACCACTTAGAGCTCCAGGTCAACCGCACCTACCAAATGCACCTTGGAGGGAAGCAGAGAGA
ATATGAGTTCTTCGGCCTGACCCCTGACACAGAGTTCCCTTGGCACCATCATGATTGCGTTCCCA
CCTGGGCCAAGGAGAGTGCCCCCTACATGTGCCGAGTGAAAGACACTGCCAGACCGGACATGGACC
TACTCCTTCTCCGGAGCCTTCCGTGTTCTCCATGGGCTTCCCTCGTCGAGTACTCTGTACCTGAG
CTACAGATATGTACCAAGCCGCTGCACCTCCCAACTCCCTGAACGTCCAGCGAGTCTGACTT
TCCAGCCGCTGCGCTTCATCCAGGAGCACGTCTGATCCCTGTCTTTGACCTCAGCGGGCCCCAGC
AGTCTGGCCCCAGCCTGTCCAGTACTCCCAGATCAGGGTGTCTGGACCCAGGGAGCCCGCAGGAGC
TCCACAGCGGCATAGCCTGTCCGAGATCACCTACTTAGGGCAGCCAGACATCTCCATCTCCAGC
CCTCCAACGTGCCACCTCCCCAGATCCTCTCCCCACTGTCTTATGCCCCAAACGCTGCCCCCTGAG
GTCCGGCCCCCATCTATGCACCTCAGGTGACCCCCGAAGCTCAATTCCCATTTCTACGCCCCACA
GGCCATCTCTAAGGTCCAGCCTTCCCTCCTATGCCCCCTCAAGCCACTCCGGACAGCTGGCCTCCCT
CCTATGGGGTATGCATGGAAGGTTCTGGCAAAGACTCCCCCACTGGGACACTTCTAGTCTCTAAA
CACCTTAGGCCTAAAGGTGAGCTTCAGAAAGAGCCACCAGCTGGAAGCTGCATGTTAGGTGGCCT
TTCTCTGCAGGAGGTGACCTCCTTGGCTATGGAGGAATCCCAAGAAGCAAAATCATTGCACCAGC
CCCTGGGGATTTGCACAGACAGAACATCTGACCCAAATGTGTACACAGTGGGGAGGAAGGGACA
CCACAGTACCTAAAGGGCCAGCTCCCCCTCCTCTCCTCAGTCCAGATCGAGGGCCACCCATGTC
CCTCCCTTTGCAACCTCCTTCCGGTCCATGTTCCCCCTCGGACCAAGGTCCAAGTCCCTGGGGCC
TGCTGGAGTCCCTTGTGTGTCCCAAGGATGAAGCCAAGAGCCCAGCCCCCTGAGACCTCAGACCTG
GAGCAGCCACAGAACTGGATTCTCTTTTCAGAGGCTGGCCCTGACTGTGCAGTGGGAGTCCCTG
AGGGGAATGGGAAAGGCTTGGTGTCTCCTCCTGTCCCTACCCAGTGTACATCCTTGGCTGTCA
ATCCCATGCTGCCATGCCACACACTCTGCGATCTGGCCTCAGACGGGTGCCCTTGAGAGAAGC
AGAGGGAGTGGCATGCAGGGCCCCCTGCCATGGGTGCGCTCCTCACCGGAACAAAGCAGCATGATA
AGGACTGCAGCGGGGAGCTCTGGGGAGCAGCTTGTGTAGACAAGCGCGTGTCTGCTGAGCCCTG
CAAGGCAGAAATGACAGTGCAAGGAGGAAATGCAGGGAACTCCCGAGGTCCAGAGCCCCACCTC
CTAACACCATGGATTCAAAGTGCTCAGGGAATTTGCCCTCTCCTTGCCCCATTCTGGCCAGTTTC
ACAATCTAGCTCGACAGAGCATGAGGCCCTTGCTCTTCTGTCTATTGTTCAAAGGTGGGAAGAGA
GCCTGGAAAAGAACCAGGCCTGGAAGAAGACAGAGGAGGCTGGGCAGAACCAGAACAACCTGC
ACTTCTGCCAAGGCCAGGGCCAGCAGGACGGCAGGACTCTAGGGAGGGGTGTGGCCTGCAGCTCA
TTCCAGCCAGGGCAACTGCCTGACGTTGCACGATTTGAGCTTCATTCTCTGATAGAACAAAGC
GAAATGCAGGTCCACCAGGGAGGGAGACACACAAGCCTTTTCTGCAGGCAGGAGTTTCAGACCTT
ATCCTGAGAATGGGGTTTGAAGGAAGGTGAGGGCTGTGGCCCCCTGGACGGGTACAATAACACAC
TGTAATGATGTACAACTTTGCAAGCTCTGCCTTGGGTTCAGCCCATCTGGGCTCAAATTCACG
CTCACCCTCACAAGCTGTGTGACTTCAAACAAATGAAATCAGTGCCAGAACCTCGGTTTCCCTC
ATCTGTAATGTGGGGATCATACACCTACCTCATGGAGTTGTGGTGAAGATGAAATGAAGTCATG
TCTTTAAAGTGCTTAATAGTGCCTGGTACATGGGCAGTGCCCAATAAACGGTAGCTATTTAAAAA
AAAAAAA

FIGURE 164

MRTLLTILTVGSLAAHAPEDPSDLLQHVKFQSSNFENILTWDSGPEGTPDPTVYSIEYKTYGERDW
 VAKKGCQRITRKSCNLTIVETGNLTLEYARVTAVSAGGRSATKMTDRFSSLQHTTLKPPDVTCIS
 KVRSIQMIVHPTPTPIRAGDGHRLTLEDIFHDLFYHLELQVNRTYQMHGKGQREYEFFGLTPDT
 EFLGTIMICVPTWAKESAPYMCRVKTLDPDRTWTYSFSGAFLFSMGFLVAVLCYLSYRYVTKPPAP
 PNSLNVQRVLTFOPLRFIQEHVLI PVFDLSGPSSLAQPVQYSQIRVSGPREPAGAPQRHSLSEIT
 YLGQPDISILQPSNVPPPQILSPLSYAPNAAPEVGPPSYAPQVTPEAQFFFYAPQAISKVQPSSY
 APQATPDSWPPSYGVCMEGSGKDSPTGTLSSPKHLRPGKQLQKEPPAGSCMLGGLSLQEVTSIAM
 EESQEAHSLHQLGICTDRTSDPNVLHSGEETPQYLKGLPLLSSVQIEGHMPSLPLQPPSGPC
 SPSDQGPSPWGLLESVLCPKDEAKSPAPETSDLEQPTELDSLFRGLALTQWES

Signal sequence.

amino acids 1-17

Transmembrane domain.

amino acids 233-250

N-glycosylation sites.

amino acids 80-83, 87-90, 172-175

N-myristoylation sites.

amino acids 11-16, 47-52, 102-107, 531-536, 565-570

FIGURE 166

MAAAPGLLFWLFWLGALWWVPGQSDLSHGRRFSDLKVCGDEECSMLMYRGKALEDFTGPDCRFVN
FKKGDDVYVYYKLAGGSLELWAGSVEHSFGYFPKDLIKVLHKYTEELHIPADETDFVCFEGGRD
DFNSYNVEELLGSLELEDSVPEESKKAEEVSQHREKSPEESRGRELDPVPEPEAFRADESDEGEA
FSESTGLQGQPSAQESHPTHSGPAANAQGVQSSLDTFEEILHDKLKVPGSESRTGNSSPASVER
EKTDAYKVLKTEMSQRGSGQCVIHYSKGFRWHQNLSLFYKDCF

Important features of the protein:

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 294-298

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34

Tyrosine kinase phosphorylation site.

amino acids 67-76

N-myristoylation sites.

amino acids 205-211, 225-231, 277-283

Amidation site.

amino acids 28-32

FIGURE 167

CCAGGACCAGGGCGCACCGGCTCAGCCTCTCACTTGTGAGAGGCCGGGGAAGAGAAGCAAAGCGC
AACGGTGTGGTCCAAGCCGGGGCTTCTGCTTCGCTCTAGGACATACACGGGACCCCTAACTTC
AGTCCCCCAAACGCGCACCCCTCGAAGTCTTGAAGTCCAGCCCCGCACATCCACGCGCGGCACAGG
CGCGGCAGGCGGCAGGTCCCGGCCGAAGGCGATGCGCGCAGGGGGTTCGGGCAGCTGGGCTCGGGC
GGCGGGAGTAGGGCCCCGGCAGGGAGGCAGGGAGGCTGCATATTCAGAGTCGCGGGCTGCGCCCTG
GGCAGAGGCCGCCCTCGCTCCACGCAACACCTGCTGCTGCCACCGCGCCGCGATGAGCCGCGTGG
TCTCGCTGCTGCTGGGCGCCGCGCTGCTCTGCGGCCACGGAGCCTTCTGCCGCCGCGTGGTTCAGC
GGCCAAAAGGTGTGTTTTGCTGACTTCAAGCATCCCTGCTACAAAATGGCCTACTTCCATGAACT
GTCCAGCCGAGTGAGCTTTCAGGAGGCACGCCTGGCTTGTGAGAGTGAGGGAGGAGTCCCTCCTCA
GCCTTGAGAATGAAGCAGAACAGAAGTTAATAGAGAGCATGTTGCAAAACCTGACAAAACCCGGG
ACAGGGATTTCTGATGGTGATTTCTGGATAGGGCTTTGGAGGAATGGAGATGGGCAACATCTGG
TGCCTGCCCAGATCTCTACCAGTGGTCTGATGGAAGCAATTCCCAGTACCGAACTGGTACACAG
ATGAACCTTCCCTGCGGAAGTGAAGAGTGTGTTGTGATGTATCACCACCAACTGCCAATCCTGGC
CTTGGGGGTCCCTACCTTTACCAGTGGATGATGACAGGTGTAACATGAAGCACAATTATATTTG
CAAGTATGAACCAGAGATTAATCCAACAGCCCCCTGTAGAAAAGCCTTATCTTACAAATCAACCAG
GAGACACCCATCAGAATGTGGTTGTTACTGAAGCAGGTATAATTCCCAATCTAATTTATGTTGTT
ATACCAACAATACCCCTGCTCTTACTGATACTGGTTGCTTTTGAACCTGTTGTTTCCAGATGCT
GCATAAAAGTAAAGGAAGAACAACAACTAGTCCAAACCAGTCTACACTGTGGATTTCAAAGAGTA
CCAGAAAAGAAAAGTGGCATGGAAGTATAATAACTCATTGACTTGGTTCCAGAATTTTGTAAATCT
GGATCTGTATAAGGAATGGCATCAGAACAATAGCTTGAATGGCTTGAAATCACAAAGGATCTGC
AAGATGAACTGTAAGCTCCCCCTTGAGGCAAATATTAAAGTAATTTTTATATGTCTATTATTTCA
TTTAAAGAATATGCTGTGCTAATAATGGAGTGAGACATGCTTATTTTGTAAAGGATGCACCCAA
ACTTCAAACCTCAAGCAAATGAAATGGACAATGCAGATAAAGTTGTTATCAACACGTCGGGAGTA
TGTGTGTTAGAAGCAATTCCTTTTATTTCTTTCACCTTTCATAAGTTGTTATCTAGTCAATGTAA
TGTATATTGTATTGAAATTTACAGTGTGCAAAAGTATTTTACCTTTGCATAAGTGTGATAAAA
ATGAACTGTTCTAATATTTATTTTATGGCATCTCATTTTCAATACATGCTCTTTTGATTAAAG
AACTTATTACTGTTGTCAACTGAATTCACACACACACAAATATAGTACCATAGAAAAAGTTTGT
TTTCTCGAAATAATTCATCTTTCAGCTTCTCTGCTTTTGGTCAATGTCTAGGAAATCTCTTCAGA
AATAAGAAGCTATTTCAATTAAGTGTGATATAAACCTCCTCAAACATTTTACTTAGAGGCAAGGAT
TGTCTAATTTCAATTGTGCAAGACATGTGCCTTATAATTATTTTACTTAAATTAACAGATT
TTGTAATAATGTAACCTTGTTAATAGGTGCATAAACACTAATGCAGTCAATTTGAACAAAAGAAG
TGACATACACAATATAAATCATATGTCTTCACACGTTGCCTATATAATGAGAAGCAGCTCTCTGA
GGGTTCTGAAATCAATGTGGTCCCTCTCTTGCCCACTAAACAAAGATGGTTGTTCCGGGTTTGGG
ATTGACACTGGAGGCAGATAGTTGCAAAGTTAGTCTAAGGTTTCCCTAGCTGTATTTAGCCTCTG
ACTATATTAGTATACAAAGAGGTCATGTGGTTGAGACCAGGTGAATAGTCACTATCAGTGTGGAG
ACAAGCACAGCACACAGACATTTTAGGAAGGAAAGGAACTACGAAATCGTGTGAAAATGGGTTGG
AACCCATCAGTGATCGCATATTCATTGATGAGGGTTTGGCTTGAGATAGAAAATGGTGGCTCCTTT
CTGTCTTATCTCCTAGTTTCTTCAATGCTTACGCCTTGTCTTCTCAAGAGAAAGTTGTAACCTCT
CTGGTCTTCATATGTCCCTGTGCTCCTTTTAAACCAATAAAGAGTTCTTGTCTTCTGGGGGAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 168

MSRVVSLLLGAALLCGHGAFRCRRVVSQGKVCFADFKHPCYKMAYFHELSSRVSFQEARLACESE
GGVLLSLENEAEQKLIESMLQNLTKPGTGISDGDGFWIGLWRNGDGQTSGACPDLYQWSDGSNSQ
YRNWYTDEPSCGSEKCVVMYHQPTANPGLGGPYLYQWDDRCNMKHNYICKYEPEINPTAPVEK
PYLTNQPGDTHQNVVVTEAGIIPNLIYVVIPTIPLLLLILVAFGTCCFQMLHKSCKGRKTSPNQ
STLWISKSTRKESGMEV

Important features of the protein:

Signal peptide:

amino acids 1-21

Transmembrane domain:

amino acids 214-235

N-glycosylation sites.

amino acids 86-89, 255-258

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 266-269

N-myristoylation sites.

amino acids 27-32, 66-71, 91-96, 93-98, 102-107, 109-114, 140-
145, 212-217